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100.0%;
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1976
691
718
1935
1038
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-07-959-946-3
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 Sequence 119, Appl Sequence 6, Appl Sequ
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Sequence 89, Appl
Sequence 111, App
Sequence 212, App
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212, App
6, Appli
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Sequence 3, Appli
Sequence 2, Appli
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Sequence 123, App
Sequence 2, Appli
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                                                                                                                               December 21, 2004, 06:53:17; Search time 38.7949 Seconds (without alignments) 456.424 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, App
Sequence 6, App
Sequence 247,
                                                                                                                                                                                                         US-09-803-918A-2
1362
1 MKAAVLTLAVLFLTGSQARH.....SFKVSFLSALBEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3,
Sequence 27
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Sequence 62
Sequence 59
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Sequence 2
Sequence 2
Sequence 2
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(/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/PcTUS COMB.pep:*

(/cgn2_6/ptodata/1/iaa/PcTUS COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-543-681A-5933
US-08-875-435B-3
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US-08-919-039-27
US-09-919-039-27
US-09-919-039-17
US-08-48-60-6
US-08-952-796-15
US-08-92-870-1
US-09-800-729-206
US-09-800-729-206
US-09-800-729-206
US-09-800-729-206
US-09-079-030-123
US-09-9750-580-3
US-09-99-360B-89
US-09-800-729-111
US-09-800-729-111
US-09-800-729-111
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                                                                                                                                                                                                                                                                                                                                              478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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28 113 9 6 574 4 US-00-462-5518-1
29 113 9 6 1130 4 US-00-462-5518-1
20 113 9 6 1130 4 US-00-462-5518-1
21 113 9 15 1100 9 15 1001 4 US-00-462-5518-1
21 113 9 15 1001 4 US-00-562-518-1
21 113 9 11 4 US-00-562-518-1
21 21 21 21 21 21 21 21 20 2 US-00-562-218-218

APPLICANT CANTERION WINDOWN LIAPER OF AUGUST AUGU
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181 DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                      61 ALGKOLNLKILDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                   121 VOPYLDDFOKKWOEEMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                               121 VÓPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                                                                             181 DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                      61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
APPLICANT: BENOTY, Patrick
APPLICANT: BENOTY, Patrick
APPLICANT: BENOTKERT, Eric
APPLICANT: DENEFUE, Patrice
APPLICANT: DUBREGRE, Nicolas
APPLICANT: TUC, Gerald
APPLICANT: TUC, Gerald
APPLICANT: TURNY, Gerd
APPLICANT: TURNY, Gerd
APPLICANT: FUNKE, Harald
APPLICANT: FUNKE, Harald
APPLICANT: FUNKE, HARALS
APPLICANT: FUNKE, HARALS
APPLICANT: FUNKE, HARALS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                          GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                                                                                                                     241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION NUMBER: WO FR96/00747
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehlmer Eeq., Paul F.
REFERENCE/DOCKET NUMBER: S135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEPAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 267 amino acids amino acids
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MOLECULE TYPE: protein
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US-08-952-796-2
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                                                                                                                                           61 ALGKOLNIKLLDNWDSVTSTFSKLREOLGPVTOEFWDNLEKETEGLROEMSKDLEEVKAK 120
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                                                1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                            1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Young, Joseph L.
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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    0; Indels
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FLLING DATE: US/08/333,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1362; DB 1; Best Local Similarity 100.0%; Pred. No. 7.1e-109; Matches 267; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dressler, Goldsmith, Shore, Sutker ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700 CITY: Chicago STATE: Illinois
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312)616-5400
TELEPAX: (312)616-5460
INPORENTION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
    Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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61 ALGKOLNLKLLDNWDSVTSTFSKLREOLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                                   1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
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PCT-US92-08634-3
Sequence 3, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Voung, Stephen G.
APPLICANT: Curtiss, Linda K.
ITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
ITLE OF INVENTION: Lipoprotein Painte and Recombinant Antigens
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: 20
ADDRESSEE: Milnamow, Ltd.
ADDRESSEE: Milnamow, Ltd.
                                                                                                                                                                                         1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                            Gaps
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                                                                                                    Length 267;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTONEX/AGBRI INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
                                                                                                Query Match 100.0%; Score 1362; DB 4; Best Local Similarity 100.0%; Pred. No. 7.1e-109; Matches 267; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. Milnamow, Ltd.
CITY: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFRAX: (312)616-5400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                   internal
         protein
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                                ; FRAGMENT TYPE:
US-08-940-136-260
              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                  121 VQPYLDDFQKKWQEEMELYRQKVBPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                                                                                                                                          121 VOPYLDDFOKKWOEEMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                                                                                                                                                                                         DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                                                                                                                                                                                                                                                                                                                 181 DALKTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                                                               9
                                                                                                                              1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
                                                                                                  1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                          Gaps
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Query Match
Best Local Similarity 100.0%; Pred. No. 7.1e-109;
Matches 267; Conservative 0; Mismatches 0: Tadele n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER: US/08/940,136
FILING DATE: APPLICATION NUMBER: OPPLICATION NUMBER: ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, LAULA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000'
TELEPHONE: 650-493-556
TELEK: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 260:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acide
TVENEY AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 260, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
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85 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                       Sequence 119, Application US/09079030
Sequence 119, Application US/09079030
Sequence 110, Application
Sequence 110, Application:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: UIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: UECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 91.1%; Score 1241; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.4e-98;
Matches 243; Conservative 0; Mismatches 0;
  241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                  ...ureSSEE: ...ureSS:
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: MCMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELEPHONE: 512/418-3000
TELEPHONE: 512/474-777
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Concurrently Herewith
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US-08-448-606-6
; Sequence 6, Application US/08448606
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                                                                 RESULT 7
US-09-079-030-119
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APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                  61 ALGKOLNIKLLDNWDSVTSTFSKLREOLGPVTOEFWDNLEKETEGLROEMSKDLEEVKAK 120
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                                                                                                                                                    1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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                                                                 Length 267;
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                                                                                                           IndelB
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OTHER INFORMATION: Incyte ID No. 6727066 2516070CD1
                                                          Query Match 100.0%; Score 1362; DB 5; Best Local Similarity 100.0%; Pred. No. 7.1e-109; Matches 267; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 98.9
Matches 264; Conservative
, MOLECULE TYPE: protein PCT-US92-08634-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-09-919-039-27
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LENGTH: 267
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TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-952-796-15
                                                                                                                                                                                                                                                                                                                                                                                                                       Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                       US-08-952-796-15
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 KAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRAR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 EGSALGKÓLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 KAKVOPYLDDFOKKWOEEMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMRDRAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKTAIAIAVALAGFATVANA-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKAAVLTLAVL---FLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQF
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91.1%; Score 1240.5; DB 1; Length 264;
Best Local Similarity 92.2%; Pred. No. 1.8e-98;
Matches 249; Conservative 3; Mismatches 9; Indels 9;
                                APPLICANT: Holmgren, Erik
APPLICANT: Mikaelsson, sa
APPLICANT: Mikaelsson, sa
APPLICANT: Sejltz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
NUMBER OF SEQUENCES:
ADDRESSEE: POLIOCK, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: S 9203753-0
FILING DATE: 11-DEC-1992
ATTONERY/AGENT INPORMATION:
WAMD: MANCHING BATE: BLACK-1992
ATTONERY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LROGLLPVLESFKVSFLSALEEYTKKLNTQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 331-711
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
Patent No. 5721114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
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68 LKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDD 127
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Sequence 15, Application US/08952796

Sequence 15, Application US/08952796

Patent No. 6258596

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: BENOIT, Patrick

APPLICANT: DUBREGER; Nicolas

APPLICANT: PRUCHART, Jean-Charles

APPLICANT: TURPIN, Gerrard

APPLICANT: TURPIN, Gerrard

APPLICANT: TURPIN, Gerrard

APPLICANT: TURPIN, Gerrard

APPLICANT: ASSWANN, Gerrard

APPLICANT: ASSWANN, Gerrard

APPLICANT: TURE HONGE, HOUSE VARIANTS OF APOLIPOPROTEIN A-I

NUMBER OF SEQUENCES: 19

CORRESPONDENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSER: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.9%; Score 1006; DB 3; Best Local Similarity 99.5%; Pred. No. 1.5e-78; Matches 199; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehlner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19426
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 SFKVSFLSALEEYTKKLNTQ 267
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US-09-800-729-206
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                                                                                                                                                                         APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                       APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AL POLYPEPTIDES, DIAGNOSTIC METHOL
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolia
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.1%; Score 328; DB 2; Length 64; Best Local Similarity 100.0%; Pred. No. 3.7e-21; Matches 64; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION 1436
PRIOR APPLICATION THREE: US/08/292,870
FILING DATE: 07-AUG-1994
APPLICATION NUMBER: US/0534,761
PRIOR APPLICATION NUMBER: US 07/534,761
PRIOR APPLICATION NUMBER: US 07/711,333
FILING DATE: 07-JUN-1991
PRIOR APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 06-JUN-1991
ATPONEY/AGENT INFORMATION:
NAME: FILLING THOMBER: 34,163
REGISTRATION NUMBER: TSRI 210.1 DI
TELECOMMUNICATION INVERMER: TSRI 210.1 DI
TELECOMMUNICATION INVERMER: TSRI 210.1 DI
TELECOMMUNICATION INVERMATION:
TELECOMMUNICATION INVERMATION:
TELEPRAK: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 207, Application US/09800729
; Patent No. 6605592
                Sequence 1, Application US/08292870 Patent No. 5814467 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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US-08-292-870-1
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61 ALGKOLNIKLIDNWDSVTSTFSKIREQIGPVTQEFWDNLEKETEGIRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.4%; Score 278.5; DB 4; Length 3
Best Local Similarity 26.1%; Pred. No. 7.2e-16;
Matches 68; Conservative 60; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 206, Application US/09800729; Sequence 206, Application US/09800729; Patent No. 6605592; GENERAL INFORMATION:
APPLICANT: Ni et al.; TITLE OF INVENTION: 32 Human secreted proteins; TILE REFERENCE: PZ044P1; CURRENT FILING DATE: 2001-03-08; PRIOR APPLICATION NUMBER: US/09/800,729; CURRENT FILING DATE: 2000-09-22; PRIOR APPLICATION NUMBER: 60/155,709; PRIOR FILING DATE: 1999-09-24; PRIOR FILING DATE: 1999-09-24; NUMBER DEGION NUMBER: 60/155,709; PRIOR FILING DATE: 1999-09-24; NUMBER DEGION NUMBER: 60/155,709; NUMBER DEGION NUMBER: 60/155,709; NUMBER DEGION NUMBER: 00/155,709; NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 128;
                       32 Human secreted proteins
241 GLLPVLESFKVSFLSALEEYT 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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60 SALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bannet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLR
   VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.9%; Score 229.5; DB 4; Length 397; 26.2%; Pred. No. 1.1e-11; ive 48; Mismatches 90; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5814467th Torrey Pines Road., TPC E
                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
ATTORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCM1lian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: AAAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/414-7577
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTER/STICS:
LENGTH: 397 amino acids
TITLE OF INVENTION: VECTORS FOR TRAINDRESER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 QGLLPVLESFKVSFLSALEEYT 261
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US-08-292-870-2
// Sequence 2, Application US/08292870
// Patent No. 5814467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.2*
Matches 53, Conservative

    Arnold, White
P.O. Box 4433

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  La Jolla
California
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                                                                                                                                                             CITY: Houston
STATE: Texas
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                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
TOPOLOGY:
US-09-079-030-123
                                                                                                                                  STREET:
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61 ALGKQLALKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                         VQPYLDDFQKKWQEEMELYRQKVBPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                           DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                                                                                                                                                                                                                          61 ALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 DVTQQLSTLFQDKLGDASTYADGVHNKLVPFVVQLSGHLAKETERVKEEIKKELEDLRDR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VOPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : : | |: : : | |: : : | 1.2 | 1.3 | 1.4 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKAAVLILAVLFLIGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 123, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044Pl
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT PILING DATE: 2001-03-08
FRIOR PRILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 SLAPLTVGVQ-----EKLNHQ 237
                                                                                                                                                                                                                                                                                                                                                                                        241 GLLPVLESFKVSFLSALEEYTKKLN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 KLNHOLEGLAFOMKKOAEELKAKIS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER. Pack
SOFTWARE: Pack
SEQ ID NO 208
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US-09-079-030-123
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Gaps

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COUNTRY: US

COMPUTER READBLE FORM:
MEDIUM TYPE: INOPPY disk
MEDIUM TYPE: INOPPY disk
COMPUTER READBLE FORM:
MEDIUM TYPE: INOPPY disk
COMPUTER: IMP Compatible
OPERATION SYSTEM: PC-COMPATIBLE
SOFTWARE: BATCHATION DATA:
FILLING DATE: US-OS/84292,870
FILLING DATE: US-OS-UNN-1991
FILLING DATE: US-UNN-1991
FILLING D
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Search completed: December 21, 2004, 07:32:17 Job time : 40.7949 secs

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5.1.6
Compugen Ltd.
 GenCore version (c) 1993 - 2004
           Copyright
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OM protein - protein search, using sw model

December 21, 2004, 06:40:58; Search time 32.2747 Seconds (without alignments) 795.975 Million cell updates/sec Run on:

Title: Perfect score:

US-09-803-918A-2 1362 1 MKAAVLTLAVLFLTGSQARH.....SFKVSFLSALBEYTKKLINTQ 267 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	apolipoprotein A-I	apolipoprotein AI	apolipoprotein A-I	apolipoprotein A-I	apolipoprotein A-I	apolipoprotein A-I		apolipoprotein A-I				apolipoprotein A-I	apolipoprotein A-1	apolipoprotein A-I	apolipoprotein E p														
SUMMARIES	ID	LPHUA1	JS0079	A26529	LPDGA1	LPRB1Z	A46018	JT0672	S31394	LPRB1B	A56858	A24998	JQ0704	\$22420	JC1237	A24700	LPCHA1	JC5456	A61448	S21830	S29565	LPHUA4	LPRTA4	C40892	B40892	A40892	A47141	A25281	JH0472	JU0036
	DB	-	~	Н	Н	-	~	N	~	Н	~	~	~	~	7	~	ч	~	~	~	~	ч	Н	~	~	7	~	~	7	7
	Length	267	267	267	266	266	265	265	264	265	265	241	231	264	262	259	264	264	246	164	429	396	391	399	391	395	401	394	258	311
d	Query Match	100.0	95.9	95.4	85.3	80.8	0	ö	79.8	79.4	٠	71.5	67.8	66.4	0.99	62.4	50.6	48.7	47.3	45.3	21.4	20.4	19.6	18.6	18.4	18.4	18.3	17.5	16.6	15.3
	Score	1362	1306	1299	1161.5	1100.5	1100	1093	1087.5	1082	1082	974.5	924	904.5	898.5	849.5	688.5	663.5	644.5	617.5	291	278.5	267	253	251	251	249.5	238.5	225.5	209
	Result No.	1	7	М	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

apolipoprotein B p	blackjack protein, apolipoprotein E p	apolipoprotein E p	apolipoprotein E -	apolipoprotein E p	apolipoprotein E p	apolipoprotein E -	apolipoprotein E p	apolipoprotein E p	apolipoprotein E -	apolipoprotein B -	apolipoprotein E p	keratin, 58K type	h-caldesmon - chic	hypothetical prote
LPRTE	T28657 A28792	803185	S33450	S12635	JC5566	C60940	LPHUE	JC6549	145996	S26478	A45951	S08381	A33430	T23512
Н (N 0	~	N	~	~	N	Н	~	N	N	N	~	н	N
312	317	317	317	298	329	291	317	316	316	316	311	513	771	470
14.5	14.3	13.9	13.8	13.5	13.4	13.1	12.8	12.2	11.7	11.7	10.8	10.7	10.5	10.1
198	194.5	189.5	188	184	182	178.5	174.5	166.5	160	160	147	146	143.5	137
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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apolipoprotein A-I precursor [validated] - human
N;Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor
S;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 09-Jul-2004
C;Accession: A90947; B90947; §02373; A93465; A21147; A93519; B93519; A93472; A94010; A2
RESULT 1
```

R.Scilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B. DNA 3, 309-317, 1984 A;Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for human A;Reference number: A90947; MUID:85026665; PMID:6207999

A;Accession: A90947 A;Molecule type: DNA A;Residues: 1-267 <SEI>

A; Accession: B90947
A; Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
A; Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
A; Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
A; Title: Sequence and expression of Tangier apoA-I gene.
A; Reference number: S02373; MUID:88196137; PMID:3129297
A; Accession: S02373
A; Molecule type: DN
A; Residues: 1.267 <AMAX.
A; Residues: 1.267 <AMAX.
A; Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729
R; Shoulders, C.C.; Kornblihtt, A.R.; Munro, B.S.; Baralle, F.E.
NuCleic Acids Res. 11, 2827-2837, 1983
A; Title: Gene erructure of human apolipoprotein Al.
A; Reference number: A93465; MUID:83220822; PMID:6406984
A; Accession: A93465

A,Molecule type: DNA
MResidues: 1-267 <SHO-)
A,Residues: 1-267 <SHO-)
A,Residues: 1-267 <SHO-)
A,Gross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; G.
R,Rarathanasis, S.K.; Zannis, V.I.; Breslow, J.L.
R;Rarathanasis, S.K.; Zannis, V.I.; Breslow, J.L.
A,Title: Solation and characterization of the human apolipoprotein A-I gene.
A,Reference number: A21147; MUID:84016011; PMID:6413973

A;Accession: A21147 A;Molecule type: DNA A;Residues: 1-267 <KAR>

A;Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AABS9514.1; PID:g178768
R;Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.B.
Nucleic Acids Res. 12, 3917-3932, 1984
A;Title: Human apolipoproteins Ai, AII, CII and CIII. cDNA sequences and mRNA abundance
A;Reference number: A93519; MUID:84221405; PMID:6328445
A;Accession: A93519
A;Accession: A93519
A;Residues: 1-267 <SHA>
A;Residues: 1-267 <SHA>
A;Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

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A;Molecule type: protein
A;Residues: 25-39 <KUN>
R;Moguilevsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.; He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: purzu
A,Reference number: 139476; MUID:89377481; PMID:2673706
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A; Residues: 1-14 < RE2>
A; Residues: 1-14 < RE2>
A; Residues: 1-14 < RE3>
A; Cross-references: GB:J04066; NID:g178763; PIDN:AAA51746.1; PID:g553183
B; Cross-references: GB:J04066; NID:g178763; PIDN:AAA51746.1; PID:g553183
B; Dischem. 54, 699-727, 1985
A; Title: Human apolipoprotein molecular biology and genetic variation.
A; Reference number: A901042; MUID:85278004; PMID:3896129
A; Contents: annotation; review of sequences, variants and gene location
B; Hosg. J. M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
A; Title: Human apolipoprotein A-1. Post-translational modification by fatty acid acylatic
A; Reference number: A92577; MUID:86140194; PMID:3005308
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A; Note: an undetermined serine or threonine is acylated by fatty acid; the acylating fat;
R; Law, S.W.; Brewer, H.B.
G; Law, S.W.; Brewer, H.B.
J. 12810-12814, 1985
A; Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.
A; Reference number: 155236; MUID:86008382; PMID:2995392
A; Title: Transient expression of wild type and mutant human apolipoprotein AI in COS cel A; Reference number: S16197; MUID: 92029676; PMID: 1930731
A; Contents: annotation; extension of studies in reference S02737
B; Stoffel, W.; Kruger, E.; Deutzmann, Y. 277-237, 1983
A; Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processing A; Reference number: A19913; MUID: 83236195; PMID: 6407957
                 COS cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Regidues: 1-6,'X',8-13,'XXX',17-18,'XX',21,'X',23-25,'X',27-29 <ST2>
R;Bhnholm, C.; Bozas, S.E.; Tenkanen, H.; Kirszbaum, L.; Metso, J.; Murphy, B.; Walker, Biochim. Blophys. Acta 1086, 255-260, 1991
A,Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein of A;Reference number: A56815; MUID:92075698; PMID:1742316
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A;Cross-references: GB:M11791; NID:g178776; PIDN:AAA35545.1; PID:g178777
C;Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
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A; Residues: 19-267 cRES>
A; Residues: 19-267 cRES>
A; Residues: 19-267 cRES>
A; Cross-references: GB W. 19069; NID:g178774; PIDN:AAA51747.1; PID:g178775
B; A; Cross-references: GB W. 19069; J. 1908
J. Biol. Chem. 263, 18530-18536, 1988
A; Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the A; Reference number: 139475; MUID:89054040; PMID:3142880
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A;Introns: 15/1; 67/2
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A; Title: Intracellular and extracellular processing of human apolipoprotein A-I: secrete A; Reference number: A21118; MUID:83195100; PMID:6405383
A; Accession: A21118
A; Accession: A21118
A; Malesidues: 1-24 < AZAN
A; Residues: 1-25 < AZAN
A; Residues: 1-27 < ARBE
A; Residues: 1-27 < AZAN
A; Residues: 1-27 ABR
A; Residues: 1
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Ajmolecule type: protein A-1 binds to a family of bovine seminal plasma proteins.
Ajmolecule type: protein A-1 binds to a family of bovine seminal plasma proteins.
Ajmolecule type: protein
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A;Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRN A;Reference number: A94010; MUID:84119464; PMID:6198645
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A; Mesidues: 25-56 eXUI.
R; Rsidues: 25-56 eXUI.
R; Nichols, W.C.; Dwulet, F.E.; Liepnieks, J.; Benson, M.D.
Biochem. Biophys. Res. Commun. 156, 762-768, 1988
A; Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
A; Reference number: A31582; MUID:89050104; PMID:3142462
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A;Residues: 25-57, Q',59-169, QQ',172-267 <BR2>
A;Residues: 25-57, Q',59-169, QQ', 172-267 <BR2>
A;Riyui, Y.; Aoyama, T.; Moribita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
Glin. Invest. 82, 803-807, 198
A;Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo. A);Reference number: A30516; MUID:88331387; PMID:3047170
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711cle: The amino acid sequence of human APOA-1, an apolipoprotein isolated from high Reference number: A90209; MUID:78123731; PMID:204308
                                                                A,Molecule type: DNA
A,Residues: 1-24 <SH2>
R;Cheung, P.; Chan, L.
Nucleic Acids Res. 11, 3703-3715, 1983
A;Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
A;Reference number: A93472; MUID:83220772; PMID:6304641
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A;Molecule type: mRNA
A;Residues: 1-267 <LAW>
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A;Molecule type: mRNA
A;Residues: 1-267 <CHE>
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Accession A-I precursor - crab-eating macaque cypecien A-I precursor - crab-eating macaque cypecien Macae fascicularis (crab-eating macaque) C;Date: 30-Sep-1989 #sequence revision 19-0ct-1995 #text_change 09-Jul-2004 C;Accession: A26529; A26677; $23135; A57766 R;Polites, H.G.; Malchior, G.W.; Castle, C.K.; Marotti, K.R. Gene 49, 103-110, 1986 Mylchior, G.W.; Castle, C.K.; Marotti, K.R. A;Accession: A26529 MUD: 87191989; PMID: 3106152 A;Accession: A26629 A;Molecule type: maxNA A;Residues: 1-267 <PODA A;Residues: 1-267 <PODA A;Residues: 1-267 <PODA A;Accession: A26627 MUD: 87184911; NID: 9342074; PIDN: AA36834.1; PID: 934207 R;Accession: A26627 A;Accession: A26627 MUD: 8718451; PMID: 3105581 A;Accession: S23135 MUD: 92305062; PMID: 1610902 A;Title: Nuclectide sequence of the cynomolgus monkey apolipoprotein A-I gene and corre-A;Accession: S23135 MUD: 92305062; PMID: 1610902 A;Accession: S23135 MUD: 92305062; PMID: 1610902 A;Accession: S23135 MUD: 92305062; PMID: 1610902 A;Accession: A;Accessi
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Kossidues: 1-10 <RES>
A;Cross-references: GB:M69223; NID:gJ42066; PIDN:AAA36831.1; PID:g553820
C;Comment: The precursor is synthesized in the liver and small intestine. The propeptid C;Comment: ApoA-I makes up about 70% of the procein of the high density lipoproteins (H) y promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin C;Genetics:
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C; Superfamily: apolipoprotein A-I
C; Superfamily: apolipoprotein A-I
C; Superfamily: apolipoprotein A-I
C; Superfamily: apolipoprotein HDL; intestine; lipid transport; plasma; tandem rep F; 1-18/Domain: signal sequence #status predicted <SIG>F; 1-18/Domain: propeptide #status predicted <PPT>F; 19-24/Domain: propeptide #status predicted <PPT>F; 25-267/Product: apolipoprotein A-I #status predicted <MAT>
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VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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Best Local Similarity 94.8%; Pred. No. 1.1e-65;
Matches 253; Conservative 6; Mismatches 8;
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                                                                                                                                       241 GLLPVLESFKVSFLSALEEYTKKLSTQ
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C;Species: Papio sp. (baboon)
C;Species: Papio sp. (baboon)
C;Species: Papio sp. (baboon)
C;Species: 31-Mar-1992 #text_change 13-Jun-1997
C;Accession: JS0079
R;Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; VandeBerg, J.L.
Gene 74, 483-490, 1988
A;Title: The baboon gene for apoliopprotein A-I: characterization of a cDNA clone and id
A;Reference number: JS0079; MUID:89232739; PMID:2907746
A;Reference number: JS0079; MUID:89232739; PMID:2907746
A;Residues: 1-267 cHIX>
A;Residues: 1-267 action of repeated amino acids which form amphipathic c;Comment: This protein contains a region of repeated amino acids which form amphipathic c;Comment: This protein contains a region of repeated amino acids which form amphipathic c;Comment: Bild binding; lipoprotein A-I
C;Reywords: HDL; lipid binding; lipoprotein
F;1-18/Domain: signal sequence #status predicted <LAI>
F;123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats
                                 C;Keywords: åtherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipid p;1spid; p;1.18/Domain: signal sequence #status experimental <51G>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-267/Product: apolipoprotein A-I #status experimental <WAT>
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                                                                                                                                                                                                    Length 267;
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Pred. No. 4.4e-66;
6; Mismatches 7;
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0
                                                                                                                                                                                                 Score 1362; DB 1;
Pred. No. 3.3e-69;
                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                   Best Local Similarity 100.0%;
Matches 267; Conservative C
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Best Local Similarity 95.1%;
Matches 254; Conservative 6
      Superfamily: apolipoprotein A-I
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A/Accession: S0664
A/Molecule type: mRNA
A/Molecule type: major component of the high density lipoproteins in plasma.
C/Comment: This protein is amajor component of the high density lipoproteins in plasma.
C/Moment: This protein the major component of the high density lipoproteins in plasma.
C/Molecter this protein the metabolism; HDL; intestine; lipid transport; plasma; tandem representationain: signal sequence #status predicted cSIG>
F/19-24/Domain: signal sequence #status predicted cSIG>
F/19-24/Domain: apolipoprotein A-I #status experimental cMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA; protein
A;Residues: 1-265 < BER>
A;Residues: 1-265 < BER>
A;Cross-references: UNIPROT:P18648; GB:L00626; NID:g164358; PIDN:AAA30992.1; PID:g164355
A;Note: sequence extracted from NCB1 backbone (NCBIN:129509, NCBIP:129511)
C;Superfamily: apolipoprotein A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein AI - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46018
R;Birchbauer, A.; Knipping, G.; Juritsch, B.; Aschauer, H.; Zechner, R.
Genomics 15, 643-652, 1993
A;Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig.
A;Accession: A46018
A;Accession: A46018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ALGKOLNIKILDINWDSVTSTFSKIREOLGPVTOEFWDNIEKETEGIROEMSKOLEEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOPYLDDFOKKWOEEMELYROKVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRARAHV 180
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Pred. No. 1.3e-54;
9; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                        80.8%; Score 1100.5; DB
80.1%; Pred. No. 1.2e-54
tive 25; Mismatches 2
      >
R;Paraskevopoulou, T.B.; Kritis, A.; Zannis, V
submitted to the EMBL Data Library, July 1989
A;Reference number: S06064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 GLLPVLESFKASVQNVLDEATKKLNTQ 266
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Best Local Similarity 80.1%
Matches 214; Conservative
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Matches 216; Conservative
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                                                                                                                                                                                                                                                                                apolipoprotein A-I precursor - dog
apolipoprotein A-I precursor - dog
C.Species: Canis lupus familiaris (dog)
R.McC C.C., Li, W.H.; Chan, L.
J. Lipid Res. 30, 1735-1746, 1989
A.Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implicati
A.Rocession: A60940
A.Rocession: A6092; MulD: 82142425; PMID: 6801039
A.Rocession: A6092; MulD: 82142425; PMID: 6801039
A.Rocession: A6092; MulD: 82142425; PMID: 6801039
A.Rocession: A6092; MulD: 82142425; PMID: 19887
A.Rocession: A61418; MulD: 76210910; PMID: 179887
A.Rocession: A61418; Accession: A6
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C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S06064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKAALLILLAVLFLTGSQARHFWQQDE - PQSPWDRVKDLATVYVDAVKDSGRDYVAQFEAS
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                                                                                                                      241 GLLPVLESFKVSFLSALEEYTKKLSTQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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A,Accession: S20557
A,Molecule type: DNA
A,Residues: 1-17,'R', 19-44,'I', 46-122,'Y', 124-146,'V', 148-265 <PAN2>
A,Cross-references: EMBL:X06659, NID:g1459; PIDN:CAA29858.1; PID:g1460
C,Comment: This protein is synthesized in the small intestine.
C,Comment: This protein is a major component of the high density lipoproteins in plasma
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A; Introns: 15/1; 66/2
C; Superfamily: apolipoprotein A-I
C; Superfamily: apolipoprotein A-I
C; Superfamily: apolipoprotein A-I
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 1-24/Domain: propeptide #status predicted <PRO>
F; 19-24/Domain: pre
                                                                                                                                                                                                                 A.; Zinke, H.; Gassen,
                                                                                                                                                                                                                                                                                         study of
                                                                                                                                                                                                                                                                                                                                                                  A, Accession: S31394
A, Status: preliminary
A, Molecule type: mRNA
A, Mesidues: 1-264 eMOE>
A, Cross-references: UNIPROT: P18648; EMBL: X69477; NID: g1889; PIDN: CAA49234.1; PID: g1890
C, Superfamily: apolipoprotein A-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų,
                                                         apolipoprotein A-I - pig
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31394
R;Moechel, B.; Flach, R.; Weiss, B.; Weiler-Guettler, H.; Frey, A.; Zinke, H.;
submitted to the EMBL Data Library, November 1992
A;Description: Genomic organization of the porcine apolipoprotein Al gene and A;Reference number: S31394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ALGKHLNLKLLDNWDSLGSTFTKVREQLGPVTQEFWDNLEKETEALRQEMSKDLEEVKKK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.8%; Score 1087.5; DB 2; Length Best Local Similarity 80.9%; Pred. No. 6.3e-54; Matches 216; Conservative 18; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 GLLPVLENLKVSILAAIDEASKKLNAQ 264
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NyAlterante names: apo-A-
NyAlterante names: apo-A-
NyAlterante names: apo-A-
NyAlterante names: apo-A-
C;Species: Sus scrofa domestica (domestic pig)
C;Dete: Sus scrofa domestica (domestic pig)
C;Dete: Sus occusion: J7672; PN0471; A65311
R;Trieu, V.N.; Patel, B.; Zhan, R.; Black, D.D.
Gene: 134, 267-70, 1993
A;Title: Sequence of the porcine apoA-I gene.
A;Recterance number: J70672; MUID:94085789; PMID:7916724
A;Accession: J70672; MUID:94085789; PMID:7916724
A;Accession: J70672
A;Accession: DNA
A;Accession: PN0471; MUID:93154581; PMID:8428656
A;Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.
A;Accession: PN0471; MUID:93154581; PMID:8428656
A;Title: Sequences and expression of the porcine apolipoprotein and c-III mRNAs.
A;Residues: 105-265 cTR2>
A;Accession: PN0471; MUID:93154581; PMID:178359
A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus A;Accession: NOS331
A;Accession: NO
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ALGKQLALKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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80.2%; Score 1093; DB 2; Length 265;
Best Local Similarity 80.1%; Pred. No. 3.1e-54;
Matches 214; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                  GLLPVLESFKVSFLSALEBYTKKLNTQ 267
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apolioporotein A-I - rabbit
apolioporotein A-I - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-1993
C;Accession: A24998
R;Yang, C. 7; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.
Eur. J. Biochem. 160, 427-431, 1986
A;Title: The primary structure of apolipoprotein A-I from rabbit high-density lipoprotein
A;Reference number: A24998; MUID:87030294; PMID:3095115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 KEGGGASLAEYQAKAREHLSVLSEKARPALEDLRQGLLPVLESFKASVQNLVDEATKKLN 239
                               VOPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                         86 EQLGPVTQEFWDNLEXETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                   DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLR
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78.5%; Pred. No. 1.1e-47;
ive 23; Mismatches 28
                                                                                                                                                                                                                                                                                                        241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                                                                               A;Accession: A24998
A;Molecule type: protein
A;Residues: 1-241 <YAN>
C;Superfamily: apolipoprotein A-I
C;Keywords: HDL; lipid binding; lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 190; Conserv
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C.Species: Bos primigenius taunus (cattle)
C.Species: Bos primigenius taunus (cattle)
C.Species: Bos primigenius taunus (cattle)
C.Gaccession: 15883; A5658 A34649
R.O.Yunigin. C.C.; Accession: 15883; A5658 A34649
R.O.Yunigin. C.C.; Chan L.: Li. M.
Wol. Biol. Evol. 7, 32-339, 139
A.Yitle: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolutic
A.Reference number: 14583; MUID: 9014478; PMID: 2117227
A.Residues: 1-255 CoMIS
A.Residues: 1-256 CoMIS
A.Residues: 1-256 A31
A.
                                                                                                                                                                                                                                                                               AFGKQLNLKLLDNWDSLSSTVSKLQEQLGPVTQEFWDNLEKETEGLREEMKKDLQEVRQK 119
                                                                                                                                                                                                                                                                                                                                                                                                                  120 VOPFLDEFOKKWOEEVERYROKVEPLGAELGESAROKLTELOEKLSFLAEELRDSARTHV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                             1 MKAVVLTLAVLFLTGSQARHFWQRDE-PRSSWDKIKDFATVYVDTVKDSGREYVAQFEAS
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                                                                                                      1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                               Gaps
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79.4%; Score 1082; DB 2; Length 265;
Best Local Similarity 78.7%; Pred. No. 1.3e-53;
Matches 210; Conservative 24; Mismatches 31; Indels
                                   Indels
   Pred. No. 1.3e-53;
; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLLPVLESFKVSFLSALEEYTKKLNTQ 267
11 Similarity 79.4%; Pre 212; Conservative 26;
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A; Accession: UC1237

A; Molecule type: DNA

A; Molecule type: DNA

A; Rossidues: 1-262 < BOY>

A; Cross-references: GB:M77801

G; Genetics: A; Gene: ApoA-I

A; Introns: 15/1; 66/2

C; Superfamily: apolipoprotein A-I

C; Superfamily: apolipoprotein A-I

C; Superfamily: apolipoprotein A-I

F; 1-24 (Domain: signal sequence #status predicted < SIG>

F; 25-262/Product: apolipoprotein A-I #status predicted < NAT>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24700; S00228; A05314
R;Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J;Biol. Chem. 261, 13268-13277, 1986
A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A;Reference number: A92558; MUID:87008540; PMID:3020028
A;Accession: A24700
A;Residues: 1-259 cHAD>
A;Residues: 1-259 cHAD>
A;Residues: 1-259 cHAD>
A;Residues: 1-259 cHAD>
A;Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
A;Reference number: S00298; MUID:84207987; PMID:6426956
A;Accession: S00298
A;Residues: 1-259 cPON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ALGKOLNIKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                             apolipoprotein A-I precursor - mouse
C;Species: Mus musculus (house mouse)
C;Accession: JO-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
C;Accession: JO-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
R;Boyle, T.P.; Marotti, K.R.
Gene 117, 243-247, 1992
A;Fitle: Structure of the murine gene encoding apolipoprotein A-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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     241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                     238 SLMPMLETLKTKAQSVIDKASSTLTAQ 264
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R) sincask, E; Hofmann, K.
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A; Reference number: $22420
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A; Molecule type: mRNA
A; Residues: 1.264
A; STO>
A; Cross-references: UNIPROT: Q00623; EMBL: X64262; NID: 950014; PIDN: CDA45560.1; PID: 950015
A; Accession: $2241
A; Molecule type: DNA
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A; Molecule type: DNA
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B; Januzzi, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setala, K.; Breslow, J.L.
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A; Molecule type: nucleic acid
A; Residues
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                             18; Mismatches
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     Pred.
79.0%;
                                Matches 184; Conservative
     Best Local Similarity
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A;Reference number: A05314
A;Reference number: A05314
A;Reference number: A05314
A;Residues: 1-18, X', 20-21, X', 23-28, X', 30-38, X', 40-41, X', 43-45 <GOR>
C;Comment: This protein is synthesized in the liver and small intestine. The propeptide c;Comment: This protein is a wajor component of the high density lipoproteins in plasma. A;Introns: 15/1; 66/2
C;Genetics: A;Introns: A;Intron
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Best Local Similarity 63.0%; Pred. No. 1.1e-40;
Matches 167; Conservative 35; Mismatches 56;
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Search completed: December 21, 2004, 07:23:19 Job time : 34.2747 secs

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December 21, 2004, 07:13:28; Search time 157.462 Seconds (without alignments) 975.635 Million cell updates/sec
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1362
1 MKAAVLTLAVLFLTGSQARH.....SFKVSFLSALEEYTKKLNTQ
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                OM protein - protein search, using sw model
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1825181 1825181 segs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Sequence:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: uniprot_sprot:*
2: uniprot_trembl:* UniProt_02:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P02647 homo sapien	Aaq91811 homo gapi	Aas68227 homo sapi	P15568 macaca fasc	Q61dn9 homo sapien	Aaa51747 homo sapi	P02648 canis famil	P18648 sus scrofa	P09809 oryctolagus	P15497 bos taurus	Q9z214 mesocricetu	O18759 tupaia glis	Q8hz96 gorilla gor	Q8hz97 pan troglod	Q8hz95 pongo pygma	Q8bpd5 mus musculu	Q00623 mus musculu	mus	mus	P04639 rattus norv	009054 rattus norv		Q8hz94 saguinus oe	Q9ts49 erinaceus e		P08250 gallus gall	P32918 coturnix co	Q7zys5 xenopus lae	Q7szal xenopus lae	Q6ddc5 xenopus tro	Q9y355 homo sapien
	OI .	APA1_HUMAN	AAQ91811	AAS68227	APA1 MACFA	Q6LDN9	AAAS1747	APA1 CANFA	APA1_PIG	APA1_RABIT	APA1_BOVIN	Q9Z2 <u>F</u> 4	APA1 TUPGB	08HZ <u>9</u> 6	Q8HZ97	Q8HZ95	Q8BPD5	APA1 MOUSE	008855	009042	APA1_RAT	009054	008877	Q8HZ94	Q9TS49	APA1_ANAPL	APA1 CHICK	APA1 COTJA	Q7ZYS5	Q7SZA1	Qeddcs	Q9Y355
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Ouerv	Match	100.0	100.0	100.0	95.9	94.1	94.1	85.3	81.1	80.8	79.1	74.3	71.6	70.6	9.07	69.5	66.5	66.4	65.8	65.7	61.9	61.4	61.2	60.4	53.4	51.8	50.6	48.7	38.6	38.1	37.6	24.0
	Score	1362	1362	1362	1306	1281	1281	1161.5	1105	1100.5	1077	1012.5	975.5	962	962	947	905.5	904.5	968	895	842.5	836	834	823	727.5	705.5	688.5	663.5	526	519	512	327
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Q61d50 mus sp. apo Aabb5539 mus sp. a Q29248 sus scrofa Q6p7h6 xenopus lae Aab61667 xenopus lae Aab59786 xenopus lae Aab59786 xenopus lae Aab59780 xenopus lae Aab59780 xenopus lae Aab59780 xenopus lae Q6fhe2 brachydanio Q6fhe2 brachydanio P06727 homo sapien Aas68228 homo sapien	
Q6LD50 AAB15539 Q29248 Q29248 G6F7H6 AAH61667 Q6FBB8 AAH59786 Q9TG6 APA4 MACFA Q6DHZ2 APA1 BRARE AAA1-1 BRARE AAA211809	
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## ALIGNMENTS

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SEQUENCE FROM N.A.
MEDLINE=80506665; PubMed=6207999;
MEDLINE=80506665; PubMed=6207999;
Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;
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                                                                                                                                                                                                                                                              "Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance.";
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'Cheung P., Chan L.;
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MEDILINES#421405; PubMed=6328445;
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Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,
Baralle F.E.;
                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=83220822; PubMed=6406984;
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       21-JUL-1986 (Rel. 01, Created)
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267 AA
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PRT;
STANDARD;
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APA1 HUMAN
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171
  TISSUESKeletal muscle;

TISSUESKeletal muscle;

TISSUESSABLATY PUBMEd=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

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SPECIES=M.fascicularis,
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Gene 49:100-110(1986)c:
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Papio hamadryas (Hamadryas baboon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
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Nickerson D.A., Smith J.D., Fullerton S.M., Buchanan A.V
Sonpar V.A., Taylor S.L., Carlson C.S., Salomaa V., Sten
Boerwinkle B., Clark A.G., Weiss K.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYSSE191; AAS68227.1;
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Biochem. Biophys. Res. Commun. 196:950-955(1993)
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181 DALRITHLAPYSDELRQRLAARLEALKENGGARLAEYHAKASEHLSTLSEKAKPALEDLRQ 240
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                                                                                                                                                                                                                                                                                                                                    61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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MEDLINE=89377481; PubMed=2673706;
MEDLINE=89377481; PubMed=2673706;
MOGUILE-89377481; PubMed=2673706;
MOGUILE-884, N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
Holmquist L., Carlson L.A., Bollen A.; Solles A., in Escherichia
"Production of human recombinant proapolipoprotein A-I in Escherichia
coli: purification and biochemical characterization.";
DNA 8:429-436(1989).
                                                                                                                                                                                                                                                                   1 MKATVLTLAVLFLTGSQARHFWQQDEPPQTPWDRVKDLVTVYVEALKDSGKDYVSQFEGS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mognilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
Holmquist L., Carlson L.A., Bollen A.;
Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases.
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                                                                                          Length 267;
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13 L -> P (in Ref. 1).
30735 MW; 869955C024088E21 CRC64;
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Last annotation update)
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                                                                                    Score 1306; DB 1
Pred. No. 5e-64;
6; Mismatches
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InterPro, IPR000074, Apolipoprotein.
InterPro, IPR009074, Apolipo A E C3.
Pfam; PF01442, Apolipoprotein; 1.
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Name=APOAl;
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   13
267 AA;
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   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        SPECIES=M.fascicularis;
MEDLINE=92305062; PubMed=1610902;
Murray R.W., Marotti K.R.;
"Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corresponding flanking regions.";
Biochim. Biophys. Acta 1131:207-210(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandeberg J.L., "The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and identification of DNA polymorphisms for genetic studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).
-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
                                                                                                                                                                                                                                                                                                  SPECIES=M.fascicularis;
MEDLINE=871865451; PubMed=3105581;
Herbort P.N., Bausserman L.L., Lynch K.M., Saritelli A.L.,
Kantor M.A., Nicolosi R.J., Shulman R.S.;
Homologues of the human C and A apolipoproteins in the Macaca
"Reactcularis (cynonolgus) monkey.";
Biochemistry 26:1457-1463(1997).
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10 X approximate tandem repeats.
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Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
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HSSP; P02647; TGW4.
InterPro; IPR000074; Apolipoprotein.
InterPro; IPR090074; Apolipop. A. E. C3.
Pfam; Pf0442; Apolipoprotein; I.
Cholesterol metabolism; Direct protein in the construction of the construc
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MEDLINE=89232739; PubMed=2907746;
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EMBL; M35634; AAA35380.1; --
EMBL; M69223; AAA36831.1; --
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199 AARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALE 258
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                                         YRQKVBPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRL
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Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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Mognilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P., Holmquist L., Carlson L.A., Bollen A.; Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases.
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249 AA; 28961 MW; COAOBOB53903FAB4 CRC64;
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EYTKKLNTQ 249
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nes 249; Conserv
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TISSUE-Heart;

X MEDLINE-98163340; PubMed-9504812;

A Dunn M.J., Corbett J.M., Wheeler C.H.;

L Electrophoresis database of dog heart proteins.";

L Electrophoresis 18:2795-2802(1997).

-!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in chylomicrons. Synthesized in the liver and small intestine.

-!- SIMILARITY: Belongs to the apolipoprotein Al/A4/E family.
                                                                                                                                                                                                                                                                                                             MEDLINE=82142425; PubMed=6801039;
Chung H., Randolph A., Reardon I., Heinrikson R.L.;
"The covalent structure of apolipoprotein A-I from canine high density
lipoproteins.";
                                                                                                                                                                                                                              C-I mRNAB:
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-57 AND 262-265.
MEDLINE=76210910; PubMed=179887;
Nakai T., Whayne T.F., Tang J.;
"The amino- and carboxyl-terminal sequences of canine apolipoprotein
                                                                                   Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                              Apolipoprotein A-I.
10 X approximate tandem repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P02647, 1AV1.

HSC-2DPAGE; P02648; DOG.

InterPro; IRR009074; Apolipoprotein.

InterPro; IRR009074, Apolipoprotein, 1.

Pfam; PF01442; Apolipoprotein; 1.

Cholesterol metabolism; Direct protein sequencing; HDL; Lipid transport; Plasma; Repeat; Signal.

SIGNAL
        21-JUL-1986 (Rel. 01, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein A-I precursor (Apo-AI).
266 AA.
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PRT;
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J. Biol. Chem. 257:2961-2967(1982).
                                                                                                                                                                                                 MEDLINE=90132271; PubMed=2515239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBBS Lett. 64:409-411(1976).
                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-266.
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TISSUE=Liver;
MEDLINE=93154581; PubMed=8428656;
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                                         Gene 123:173-179(1993)
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                                                                                                            1 MKAALLILAVLFLIGSQARHFWQQDE-PQSPWDRVKDLATVYVDAVKDSGRDYVAQFEAS
                                                                                                                                    61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                            121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV
                                                                                                                                                                                                     DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiler-Guettler H., Sommerfeldt M., Papandrikopoulou A., Mischek U., Bonttz D., Frey A., Grupe M., Scheerer J., Gassen H.G.; "Synthesis of apolipoprotein A-1 in pig brain microvascular endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-93224154; PubMed=8468059; Birchbauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.; "Characterization of the apolipoprotein AI and CIII genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression of apolipoprotein A-I in porcine brain endothelium in
                                                                                   ä
                                                                   DB 1; Length 266;
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MEDLINE=94125128; PubMed=8294940;
Moeckel B., Zinke H., Flach R., Weiss B., Weiler-Guettler H.,
                                                                                  20; Indels
                A -> G (in Ref. 2).

B -> Q (in Ref. 2).

E -> Q (in Ref. 2).

NQ -> A (in Ref. 3).

A3202620C28A869D CRC64;
                                                                 85.3%; Score 1161.5; Di
85.0%; Pred. No. 4e-56;
iive 19; Mismatches ;
                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-FPB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
09-JUL-2004 (Rel. 44, Last annotation update)
Name=APOAl;
(half-length).
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MEDLINE=90132667; PubMed=2105375;
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                                                  30196 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 domestic pig.";
Genomics 15:643-652(1993).
                                                                Query Match
Best Local Similarity 85.0*
Matches 227; Conservative
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242
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266 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.; "Sequences and expression of the porcine apolipoprotein A-I and C-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erythrocebus pates monkey.";
Biochemistry 15:1928-1933(1976).
-!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in chylomicrons. Synthesized predominantly in the intestine and the
                                                                                                                                                                                                                                                                                                                                                                                                                           Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.; "Characterization of the plasma lipoproteins and apoproteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein A-I.
10 X approximate tandem repeats.
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                                                                                                                                                                                                             B.P., Trieu V.N.,
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Missing (in Ref. 2 and 3).
D -> S (in Ref. 4).
E -> A (in Ref. 2 and 3).
HV -> QL (in Ref. 1 and 5).
G -> D (in Ref. 2 and 3).
A -> G (in Ref. 4).
W, 2C6ES78318ECF69C CRC64;
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InterPro; IPR000074; Apolipo A E C3.
Pfam; PF01442; Apolipoprotein; 1.
Cholesterol metabolism; Direct protein sequencing; HDL;
Lipid transport; Plasms; Repeat; Signal.
SIGNAL

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By similarity.
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                                                                                                                                                                            SEQUENCE OF 25-265.
Haeler-Rappez J.O., Chaudhary R., Chowdhary
Adokson K., Gustavsson I., Rapacz J.;
Submitted (OCT-1995) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X17057; -; NOT ANNOTATED CDS.
EMBL; X59414; CAA42050.1; -.
PIR; A46018; A46018
PIR; A170672, 170672.
PIR; S21830; S21830.
PIR; S31394; S31394.
HSSP; P02647; 1AV1.
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MEDLINE=76184721; PubMed=178359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
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2; CAA29858 and 3).
2; CAA29858/CAA29857).
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2; CAA29858/CAA29857)
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Missing (in Ref. 3; CAA29858).

E -> Q (in Ref. 2; CAA29858).

Y -> F (in Ref. 2; CAA29857).

Y -> F (in Ref. 2; CAA29857).

A -> V (in Ref. 2; CAA29858 and

R -> G (in Ref. 2; CAA29858/CAA

N -> Q (in Ref. 2; CAA29858/CAA

N -> Q (in Ref. 3; CAA29858/CAA

S -> K (in Ref. 2; CAA29858/CAA

VL -> LV (in Ref. 3).

L -> V (in Ref. 2; CAA29858/CAA
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ag 27; Indels
                                                                                                               InterPro; IPR000074; Apolipoprotein.
InterPro; IPR000074; Apolipop. A. E. C3.
Pfam; PF01442; Apolipoprotein; Cholestero, metabolism; Direct protein sequencing; HDL; Cholestero, Plasma; Repeat; Signal.
SiGMAL 19 24
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OFF6DB386497C7D2 CRC64;
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 nodified and this statement is not removed.
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; Pred. No. 8.6e
25; Mismatches
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(Rel. 22, Last sequence update)
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             entities requires a license agreement (or send an email to license@isb-sib.ch)
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                                                 EMBL; X15908; CAA34024.1; -. EMBL; X06658; CAA29857.1; -. EMBL; X06659; CAA29858.1; -. PIR; S06064; LPRBIZ. HSSP; P02647; LAVI.
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80.1%;
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Best Local Similarity 80.1%
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P15497;
01-APR-1990
01-MAY-1992
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                                                                                                    ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                               1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV
                                                                                                                                                                             VOPYLDDFONKWOEEMETYROKMAPLGAEFREGAROKVOELOEKLSPLAEELRDRLRAHV
                                                                                                                                                                                                      | DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L., Kroon P.A., Chao Y.S.; Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-I is synthesized in the intestine but not in the
                          ..
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the apolipoprotein Al/A4/E family.
81.1%; Score 1105; DB 1; Length 265; 80.9%; Pred. No. 4.9e-53;
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=22AP AI; TISSUE=Small intestine;
Paraskevopoulou T.B., Kritis A., Zannis V.I.;
Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases
                         29;
                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 13, Last sequence update) (Rel. 44, Last annotation update)
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                         20; Mismatches
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                                                                                                                                                                                                                                                                        Apolipoprotein A-I precursor (Apo-AI).
                                                                                                                                                                                                                                                         GLLPVLESFKVSFLSALEEYTKKLNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 170:99-104(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Intestine;
MEDLINE-88082866; PubMed=3121329;
                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
                        Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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             Similarity
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05-JUL-2004 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
     Best Local Simi
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=APOA1;
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 Query Match
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120

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Query Match
Best Local Similarity 78.74
Matches 210; Conservative
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SEQUENCE 2
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Matches 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).

-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
                                                                                                                                                                                                                                                                                                                                     MEDLINE=90147795; PubMed=2105728;
Aubolron S., Sparrow D.A., Beaubatie L., Bauchart D., Sparrow J.T.,
Laplaud M.P., Chapman J.M.;
"Characterization and amino-terminal sequence of apolipoprotein Alfrom plasma high density lipoproteins in the preruminant calf, Bos
                                                                                                                                                                                                                              MEDLINE=92153895; PubMed=1739745; Sparrow D.A., Lee B.R., Laplaud M.P., Auboiron S., Bauchart D., Chapman J.M., Gotto A.M. Jr., Yang C.Y., Sparrow J.T.; Chapman Jipid transport in the preruminant calf, Bos spp: primary structure of bovine apolipoprotein A-I."; Biochim. Biophys. Acta 1123:145-150(1992).
                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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10 X approximate tandem repeats.
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                                                                                                                                                                CDNA
                                                                                                                                   MEDLINE=90348478; PubMed=2117227;
O'Huigin C., Chan L., Li W.H.;
Cloning and sequencing of bovine apolipoprotein A-I cDN
molecular evolution of apolipoproteins A-I and B-100.";
Mol. Biol. Evol. 7:327-339(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P02647; 1AVI.
InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo_A_E_C3.
Pfam; PF01442; Apolipoprotein; 1.
Cholesterol metabolism; Direct protein sequencing; HDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --> HV (in Ref. 2).
06A2681EA2ABA50F CRC64;
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  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipid transport; Plasma; Repeat; Signal.
SIGNAL 18
05-JUL-2004 (Rel. 44, Last annotation of Apolipoprotein A-I precursor (Apo-AI). Name-APOA1; Bos taurus (Bovine).
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                                                                                             NCBI_TaxID=9913;
                                                                                Bovinae; Bos
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CONFLICT
SEQUENCE
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                                                                                                                                                                              61 ALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                             1 MKAVVLTLAVLFLTGSQARHFWQQDD-PQSSWDRVKDFATVYVEAIKDSGRDYVAQFEAS
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                                                                                          MKAAVLTLAVLFLTGSOARHFWOODEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Length 265;
                                            32; Indels
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Last annotation update)
; Score 1077; DB 1;
; Pred. No. 1.7e-51;
23; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008289; F:lipid binding; IEA.
GO; GO:0068689; P:lipid transport; IEA.
InterPro; GO:0000809; P:lipoptocein metabolism; IEA.
InterPro; IPR000074; Apolipoprocein.
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79.1%;
78.7%;
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60 ALGKQLNLKLVDNWDTLGSTFQKVHEHLGPVAQBFWEKLEKETBELRREINKDLEDVRQK 119
                                                                                                                                                                                                                           120 TQPFLDEIQKKWQEDLERYRQKVEPLSAQLREGARQKLMELQEQVTPLGEDLRDSVRAYA 179
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                                                                                                                 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                      1 LATVYVDVLKDSGRDYVSQFEGSALGKQLMLKLLDNWDSVTSTFSKLREQLGPVTQEFWD 60
                             MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY092008; AAM76625.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008289; P:lipid binding; IEA.
GO; GO:0006689; P:lipid transport; IEA.
GO; GO:0006689; P:lipid transport; IEA.
GO; GO:0006689; P:lipid transport; IEA.
InterPro; IRR009074; Apolipoprotein.
InterPro; IRR009074; Apolipoprotein.
FEGN: Apolipoprotein.
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Last annotation update)
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Gorilla gorilla (gorilla).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipid transport; Plasma; Repeat; Signal.
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Mammalia, Eutheria, Scandentia, Tupaiidae, Tupaia.
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10 X approximate tandem repeats.
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69.7%; Pred. No. 5.9e-46;
ive 38; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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3 (half-length)
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By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pupaia glis belangeri (Common tree shrew)
                                                                                                                                                                                  241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein A-I precursor (Apo-AI). Name=APOAl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo A E C3.
Pfam; PF01442; Apolipoprotein; I.
Cholesterol metabolism; HDL; Lipid tr
                                                                                                                                                                                                                                                                                                              PRT;
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HSSP; P02647; 1AV1.
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Best Local Similarity 69.7%
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
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243
265 AA;
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Pongo pygmaeus (Orangutan).
Pongo pygmaeus (Orangutan).
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
NCBI_TaxID=9600,
                                                                                                    Pan troglodytes (Chimpanzee).

Eukaryota, Metazoa, (Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Pan.
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A C'húigin C., Tichy H., Klein J.;
E SUBL; AY092009; AAP16261.j. -.
R GO; GO:0008289; P:lipid binding; IEA.
R GO; GO:0008869; P:lipid transport; IEA.
R GO; GO:0042157; P:lipoprotein metabolism; IEA.
R InterPro; IPR000074; Apolipoprotein.
R InterPro; IPR009074; Apolipoprotein.
R Pfam; PF01442; Apolipoprotein; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.6%; Score 962; DB 2; Length 191; 99.0%; Pred. No. 2.38-45; 1ive 0; Mismatches 2; Indels
                                                                                                                                                                                      A SEQUENCE FROM N.A.

O'huigin C., Tichy H., Klein J.;
O'huigin C., Tichy H., Klein J.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY092007; AAA76624-1;
R GO; GO:0008289; F:lipid binding; IEA.
GO; GO:004289; F:lipid binding; IEA.
GO; GO:0042157; P:lipidite transport; IEA.
R GO; GO:0042157; P:lipidite transport; IEA.
R GO; GO:0042157; P:lipoprotein metabolism; IEA.
R InterPro; IPR000074; Apolipoprotein.
R InterPro; IPR009074; Apolipoprotein.
R PIAM; PF01442; Apolipoprotein; I.
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191 AA; 22087 MW; 2D30919874C8F0F4 CRC64;
                                                               Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                  Created)
                PRT;
                                                                                                 Apolipoprotein A-I (Fragment).
                                             01-MAR-2003 (TrEMBLrel. 23, 0
01-MAR-2003 (TrEMBLrel. 23, 1
01-MAR-2004 (TrEMBLrel. 26, 1
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Best Local Similarity 99.0
Matches 189; Conservative
                PRELIMINARY;
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121 LHELHEKLSPLGEEXRDRARAHVDALRTHLAPYTDELRQRLAARLEALKENGGARLAEYH 180
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                                                                                                                    69.5%; Score 947; DB 2; Length 191; 96.9%; Pred. No. 1.5e-44; tive 3; Mismatches 3; Indel8
                                                                    191 AA; 22128 MW; D8D0671444C13725 CRC64;
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                                                                                                                    Query Match
Best Local Similarity
Lipoprotein.
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Human lip
Human apo

Abg97587
Abg97683
Abg97886
Abg97602

ALIGNMENTS

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Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA fragment in cloning site downstream of expression vector promoter and introducing into host microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human apolipoprotein may be produced by a suitable transformed host, it is effective in treating hyperlipaemia and arteriosclerosis. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKAAVLTIAVLFLTGSQARHFWQQDEPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assumed human apolipoprotein A-1 derivative gene product.
                         ABG97603
ABG97586
ABG97586
ABG97602
ABG97601
ADD29962
ABG97589
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(first entry)
WPI; 1986-165025/26.
N-PSDB; AAN60886.
Sequence 267 AA;
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07-OCT-1991
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Aao15892 Human apo
Aby7593 Human apo
Aby7693 Human apo
Aby7695 Human apo
Aby7665 Human apo
Adi19765 Human apo
Adi19762 Human APO
Adi19762 Human APO
Adi19762 Human apo
Adi19762 Human hea
Adi83083 Human pro
Adi83083 Human pro
Adi83084 Recombina
Ady83084 Human pro
Ady830866 Recombina
Ady83086 Apolipopr
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Ady83086 Apolipopr
Ady83086 Apolipopr
Ady83087 Carab-eati
                                                                                          December 21, 2004, 06:24:01; Search time 159.744 Seconds (without alignments) 599.590 Million cell updates/sec
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                                                                                                                                                            1362
1 MKAAVLTLAVLFLTGSQARH......SFKVSFLSALBBYTKFLNTQ
              GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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AAB47620
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AAR34032
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geneseqp2003as:*
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Maximum DB seq length: 200000000
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AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its corresp. CDNA, including presignal residues and propeptide residues. according to Seilhamer et al., DNA 3(1:309 (1984). A dispersible apo A-I/B-100 fusion polypeptide is claimed which contains a first AA sequence of apo A-I and that includes at least AA sequence positions 120-135 (see AAR72606) and which reacts with pan anti-apo AI antibodies such as: AI-4 ATCC HB8744; AI-7 ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI
                             ALGKOLNIKILLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                  61 ALGKOLNIKLIDNWDSVTSTFSKLREQIGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                           VQPYLDDFQXKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                         DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                                                                                           DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO 240
1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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/label= claimed
/note= "as part of fusion polypeptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide mimic of native apo B-100 and assays for LDL and HDL in plasma samples.
                                                                                                                                                                                                                      GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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/label= claimed
/note= "as part of
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'label= presignal
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/label= I
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                                                                                                                                            ALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                               VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                          human preproapoprotein A1; high density lipoprotein deficiency; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= propeptide
25. .267
/label= mature apoprotein
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|label= precursor
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N-PSDB; AAN82064.
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(BOLL/) BOLLEN A.
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24-OCT-1990
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MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS

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Dasseux J, Sekul R,
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SEKUL R.
BUTINER K.
CORNUT I.
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                                                           Sequence 267 AA;
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(SEKU/)
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(DUFO/)
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(CORN/)
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                                                                                                                             120
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                                                                                                                                                                                                                     DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
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-11 ATCC HB 9201; Ai-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB 9204; AI-18 ATCC HB 9507
                                                                                                                                      ALGKQLNLKILDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
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                                                                                                         MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                             ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQFFWDNLEKETEGLRQEMSKDLEEVKAK
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                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
                                                 ; Score 1362; DB 2;
; Pred. No. 3e-99;
0; Mismatches 0;
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100.0%;
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92US-00901706.
92US-00959946.
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                                              Query Match
Best Local Similarity 100.
Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                                                                      (revised)
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence of apo AI
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                               Sequence 267 AA;
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18-JUN-1992;
08-OCT-1992;
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13-AUG-1993
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acid residue sequence up to 250 residues in length that includes residues 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375 residues in length that includes residues 217-297 of apo B-100 and DNA encoding it. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ALGKQLNLKLLDNWDSVTSTFSKLRRQLGPVTQEFWDNLEKRTFGLRQEMSKDLBEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
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                                                                                                                                                                                                                Length 267;
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                                                                                                                                                                                                          Query Match 100.0%; Score 1362; DB 2; Best Local Similarity 100.0%; Pred. No. 3e-99; Matches 267; Conservative 0; Mismatches 0;
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90. .111
/note= "Involved in lectin-cholesterol acyltransferase
                        74. 111
/note= "Involved in lipoprotein-mediated cholesterol
efflux from monocytes"
                                                                                                                                         Major antigenic epitope domain
                                                                                                                                                                                                                                                     .56. .267
|Jabel= AFTI
|note= "13 kD C-terminal fragment"
                                                                                                                                                                                                                                         Receptor binding domain
                                                                                                                                                                                                                Amphipathic helix
            label= Amphipathic helix
                                                                                                                                                               label= Amphipathic helix
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                                                                                                               Hinged domain
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/label= Pr
56.
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'label= Am
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/label= Ma
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/label= Am
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                                                                                        activity"
                                                                                                     ,9. .143
'label= H
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
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     The present invention describes a nucleic acid (A) encoding an apolipoprotein A-1 (apoA-1) agonist (B) that is a peptide, or analog, which forms an amphipathic alpha-helix in presence of lipids. (A), optionally as a complex with lipids, and host cells that contain (A), are useful for gene therapy, or prevention, of diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenoiss, HDL (high density lipoprotein) and apoA-1 deficiency, hypertriglyceridemia and metabolic syndrome, also to treat endotoxemia (septic shock). Host cells containing (A) can also be used to study the role of apoA-1 in lipid metabolism. (B) can also be used to study the role of apoA-1 in lipid metabolism. (B) can be used diagnostically, e.g. to measure serum HDL (particularly its subpopulation involved in retrograde cholesterol transport) and for imaging the circulatory system or HDL accumulations at fatty streaks. The present sequence represents human apoA-1
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                                                                                                                                                                                                                                                                                                                   ALGKOLNLKLILDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                 DALRTHLAPYSDELRQRLAARLEALKENGGARLAESYHAKATEHLSTLSEKAKPALEDLRQ
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/label= Phylogenetically conserved domain
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/label= Helical lipid binding domain
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/label= AFTI
/note= "13 kD N-terminal fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= AFTI
/note= "18 kD N-terminal fragment"
                                                                                                                                                                                                                Query Match 100.0%; Score 1362; DB 2; Best Local Similarity 100.0%; Pred. No. 3e-99; Matches 267; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Amphipathic helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkinson's disease; psoriasis; probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB47620 standard; protein; 267 AA.
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This sequence shows full length apolipoprotein (Apo-Al). Fragments of Apo-Al may be used as Apo-A-I fragment T-cell activation inhibitors (AFT1). These fragments are selected from an 18 KD N-terminal fragment (amino acids 25-194), a 13 KD N-terminal fragment (amino acids 25-194), a 13 KD N-terminal fragment (amino acids 25-194) and a 13 KD C-terminal fragment (amino acids 25-194) and a 13 KD C-terminal fragment (amino acids 25-194) and a 13 KD C-terminal fragment (amino acids 15-267). The AFTI polypeptides and polynucleotides are useful for regulating T-cell mediated activation of monocytes and for treating, diagnosing, ameliorating diseases associated with IL-1 and/or TNF activity. The diseases are acute pancreatitis, Alzheimer's disease, asthma, cancer, fever, inflammatory bowel disease, ischemia, multiple sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous examples of other diseases are given in the specification. The AFTI nucleic acids are useful as hybridization probes in diagnostic assays to test for the presence of an AFTI or Apo-A-I DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apo-A-I fragment T-cell activation inhibitor (AFT1) polynucleotides, useful for treating, diagnosing, ameliorating diseases associated with IL-1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1362; DB 4; Length 267;
Pred. No. 3e-99;
'label= Helical lipid binding domain
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                                                                                                        /label= Amphipathic helix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A; 132pp; English.
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human protein that is associated with high serum cholesterol, low serum
                                                                                                                                                                                                                                                                                                   VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein analogue; Apo A; arteriosclerosis; endotoxin removal; angina pectoris; myocardial infarction; arterial stenosis; claudicatio; carotis stenosis; cerebral arterial stenosis; gene therapy; cholesterol; cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel apolipoprotein construct comprising apolipoprotein A linked to carbohydrate, peptide or protein heterologous group, useful for treating plaque/unstable angina pectoris, myocardial infarction, arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an Apolipoprotein (Apo) construct (I) for use a medicament having general formula apo-A-X, where apo-A is an apolipoprotein AI, AII or AIV, or its
                                                                                                                                                                                                        ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                                                                                                                                                     VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV
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                                                                                                                                             MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                                                          1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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                                                                              Length 267;
                                                                            Score 1362; DB 5; Length
Pred. No. 3e-99;
0; Mismatches 0; Indels
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                 HDL and/or cardiovascular disease
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                                                                              100.08;
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15-JAN-2001; 2001DK-0000057.
26-JAN-2001; 2001US-0264022P.
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                                                                  Query Match
Best Local Similarity 100.
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                                                Sequence 267 AA;
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                                                                                                                                                          180
                                                                                                                                                                                                                        240
                                                                                                             ALGKOLNIAKLIDNWDSVTSTFSKIREQIGPVTQEFWDNLEKETEGIRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene therapy; single nucleotide polymorphism; SNP; expedirome C oxidase subunit VIb; COX6B; high serum cholesterol; GPI-1; N-acetylglucosaminyl transferase component; cardiovascular disease; HDL; glycosylphosphatidylinositol-1; low serum high density lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting the presence or absence of an allelic variant of a polymorphic region of COX6B and/or GPI-1 gene, useful for detecting a predisposition to high serum cholesterol, low serum HDL and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention comprises methods of detecting the presence or absence of
                                                  ALGKOLNIKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                                          VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKL,SPLGEEMRDRARAHV
                                                                                                                                                                                                                      DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
                              MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
   Gaps
   ;
   IndelB
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 Mismatches
                                                                                                                                                                                                                                                                                  GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                                                                                                                                                                    Disclosure; Page 137-138; 199pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human apolipoprotein A-1 (APOA1).
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                                                                                                                                                                                                                                                                                                                                                                                               AA015892 standard; protein; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kleyn PW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001; 2001US-00802640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braun A, Bansal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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267;
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26-OCT-2001; 2001US-0335075P.

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analogue or variant, and X is heterologous group e.g., amino acid, peptide, protein, carbohydrate or a nucleic acid, providing that when (I) consists of exactly two identical, native apolipoproteins these are inked serially. (I) is useful for preparing a pharmaceutical composition which further comprises excipients, adjuvants, additives, such as phospholipids, cholesterol or triglycerides. (I) is useful or treating and/or preventing arteriosclerosis, for removing endotoxins, for treating and/or preventing alteriosclerosis, for removing endotoxins, for treating and or preventing plaque or unstable angina pectoris, myocardial infarction, arterial stenoses such as claudicatio, carotis srenosis.

C cerebral arterial stenoses such as claudicatio, carotis srenosis, cerebral arterial stenoses such as claudicatio, carotis srenosis, correbral arterial stenoses such as claudicatio, carotis srenosis.

C cerebral arterial stenoses such as claudicatio, carotis srenosis, correbral arterial stenoses and or unstable of a cerebral attenial genome for interespondance of a native apoA-1, A-11 or A-1V, preferably two times higher or more preferably 10 times higher than the half-life of the compared to native apoA-1, A-11 or A-1V, (I) causes substantially no immune response in humans. This is the amino acid sequence of a human
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/note= "wild-type Leu can be replaced with Pro"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1362; DB 5;
; Pred. No. 3e-99;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               apolipoprotein (Apo) analogue fragment
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Best Local Similarity 100.
Matches 267; Conservative
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Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 267 AA;
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The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polynucleotide is useful for preparing a composition for treating cardiovascular disorder. The present sequence represents a human ApoA-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                 1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                           New Apoliprotein A-1 mutation, useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atherosclerosis; pro-atherogenic inhibitor; antiatherosclerotic; macrophage-specific expression element; gene therapy; apolipoprotein;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1362; DB 6; Length 267; 100.0%; Pred. No. 3e-99; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apoplipoprotein (APOA1) protein SEQ ID NO:10.
                                                                      Hayden MR;
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                                                                      Samuels M,
                                                                                                                                                            cardiovascular disorder.
                                                                                                                                                                                         Claim 19; Page 33; 52pp; English.
                          (XENO-) XENON GENETICS INC. (UYBR-) UNIV BRITISH COLUMBIA.
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                                                                                                                                                                                                                                                                                                                                                                      Matches 267; Conservative
                                                                      Dube M,
                                                                                                  WPI; 2003-449258/42.
N-PSDB; ACC48172.
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                 wild-type protein
                                                                                                                                                                                                                                                                                                           Sequence 267 AA;
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                                                                      Brownlie AJ,
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The present invention describes a nucleic acid (I) comprising a nucleotide sequence encoding an inhibitor of a pro-atherogenic molecule operationally linked to a macrophage-specific expression element. Also described: (I) a vector (II) comprising (I); (2) an embryonic stem cell (III) comprising (I); (3) an isolated mammalian cell (IV) comprising (I); (4) a recombinant cell (V) comprising a macrophage expressing nucleic acid encoding an inhibitor of a pro-atherogenic molecule; (5) a transgenic non-human mammal (VI) comprising recombinant cells containing a transgenic nucleic acid encoding an inhibitor of a pro-atherogenic molecule; and (6) a non-human mammalian cell (VII) isolated from (VI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (I) has antiatherosclerotic activity and can be used in gene therapy. (I) or (V) can be used for inhibiting or reducing atherosclerosis, by administering to an individual (I) or apopulation of (V), where the population of (V) is derived from leukcytes, monocytes, macrophages or stem cells. (V) or (VI) is useful to screen for a drug potentially effective for treating atherosclerosis. (V) is useful for identifying a compound that reduces susceptibility to developing atherosclerosis. (V) is useful for identifying a neglul for determining the role of an inhibitor of pro-atherogenic model for atherosclerosis used in drug developing to condition of an animal model for atherosclerosis used in drug development. The present sequence represents human apolipoprotein (APOAI), which is given in the
                                                                                                                                                                                                                                                                                        Novel nucleic acid useful for inhibiting or reducing atherosclerosis, comprises nucleotide sequence encoding an inhibitor of a pro-atherogenic molecule operationally linked to a macrophage-specific expression
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                                                                                                                      WPI; 2003-201457/19.
                                                                                                                                                                              N-PSDB; ABZ59334
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Davis RA;
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                                                                                                                                                          ALGKQLNLKLLDNWDSVTSTFSKLRRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                    MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                       ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                                                                                        VQPYLDDFQKKWQBEMELYRQKVBPLRABLQEGARQKLHELQEKLSPLGEEMRDRARAHV
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                                                                   1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                        Gaps
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100.0%; Score 1362; DB 6; Length 267; 100.0%; Pred. No. 3e-99; or Indels 0;
                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          GLLPVLESPKVSFLSALEEYTKKLNTQ 267
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                    Best Local Similarity
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Human apolipoprotein A-1 (apo-A-1).
                   ADA61214 standard; protein; 267
                                                          20-NOV-2003 (first entry)
                                       ADA61214;
RESULT 11
           ADA61214
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Score 1362; DB 6; Length 267; Pred. No. 3e-99;

100.0%;

Best Local Similarity

Query Match

Sequence 267 AA;

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The invention discloses a apolipoprotein A-I (apo-A-I) polypeptide or its related polypeptide, apo-A-I fragment T-cell activation inhibitor-like (AFTI) polypeptide, or a fragment or an allelic or splice variant. Apo-A-I and its derivatives are used in regulating T-cell-mediated activation of monocytes. Also disclosed is an antibody produced by immunising an animal with apo-A-I and a selective binding agent, or its fragment. Apo-A-I is useful for reducing inflammation, interleukin (IL) labeta secretion or trumour necrosis factor (TNP)-alpha secretion in a subject, or for compositions of the invention are useful for treating (e.g. gene compositions of the invention are useful for treating (e.g. gene charapy), preventing or ameliorating a medical condition involving monocyte activation in a patient, for determining whether a compound inhibits activity or production of apo-A-I, for detecting or quantifying the amount of apo-A-I in a sample, for requlating T-cell-mediated conting AFTI receptors, and estable conting AFTI receptors, and estable conting AFTI receptors, and as an immunogen to raise antibodies, for treating acute and chronic IL-1 mediated diseases such as acute pancreatitis, Alzheimer's disease, content diseases such as depression, pancreatitis, and acute and chronic TNF-mediated diseases such as depression, pancreatitis, and acute and chronic TNF-mediated diseases such as depression, pancreatitis, and acute pancreatisis, reperfusion injury, theumatic and chronic and chronic TNF-mediated diseases such as depression, pancreatitis, and each and chronic and chronic and chronic and particular and are and chronic and chronic and chronic and chronic and acute and chronic and chronic and chronic and chronic and chronic and acute and chronic and chronic and acute and chronic and acute and chronic and acute and chronic and acute and acu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New apolipoprotein A-I polypeptide or its related polypeptide termed apo-
A-I fragment T-cell activation inhibitor-like polypeptide, useful for
treating interleukin-1 or tumor necrosis factor-alpha mediated disease.
                                                                                                           cancer; diabetes; glomerulonephritis; multiple sclerosis; osteoporosis; apain; Parkinson's disease; psoriasis; uveltis; TMF mediated disease; depris pancreatitis; periodontal disease; pulmonary fibrosis; reperfusion injury; rheumatic disease; septic shock; systemic lupus erythematosus; thyroiditis; noctropic; neuroprotective; cytostatic; nephrotropic; analgesic; ophthalmological; antiinflammatory; vasotropic; antibacterial; immunosuppressive; dermatological.
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Human; apolipoprotein A-I; apo-A-I; T-cell activation inhibitor-like; AFTI; T-cell-mediated activation; monocyte; interleukin-lbeta; IL-lbeta; tumour necrosis factor alpha; TNF-alpha; gene therapy; IL-lmediated disease; acute pancreatitis; Alzheimer's disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards CK;
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BURGER D.
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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(BURG/)
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                                                                                                                                                                                                                                                                                                                                         antiallergic, antinflammatory; respiratory; antiarthritic; dermatological; antibacterial; cerebroprotective; vasotropic; cardiant; haemostatic; hypotensive; hepatotropic; neuroprotective; anorectic; nootropic; antibucer; muscular; immunosuppressive; gynaecological; antipsoriatic; endocrine; ophthalmological; osteopathic; antipsoriatic; endocrine; ophthalmological; osteopathic; antifactulity; antilipaemic; cardiomyopathy; atheroscierosis; diabetes; cell signal processing; metabolic pathway; asthma; allergy; emphysema; autoimmune; graft-versus.host; arthritis; cancer; stroke; haemophila; obesity; Alzheimer's; pain; chromosome mapping; tissue typing; human; apolipoprotein A-I precursor.
                                                           ALGKQLNLKILDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                      61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                     121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                           DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO 240
                    9
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                   1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                        DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO
                                 1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
Gaps
                                                                                                                                                                                                                                                                                                                                  cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic;
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 Indels
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Mismatches
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2001US-0309247P
2001US-0311754P
2001US-0313331P
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2001US-0269940P.
2001US-0274192P.
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2001US-0279840P.
2001US-0282981P.
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267; Conservative
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ZERHUSEN B D
PATTURAJAN M
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08-MAR-2001; 2
22-MAR-2001; 2
29-MAR-2001; 2
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17-AUG-2001;
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(PATT/)
(LEPL/)
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(LIUX/)
(SPYT/)
Matches
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The invention relates to a novel isolated NOVX polypeptide. The polypeptide demonstrates cytostatic, antiarteriosclerotic, antidiabetic, antialtathmatic, antiallergic, antialfalmamatory, respiratory.

antiarthmatic, dermatological, antibacterial, cerebroprotective, cardiant, haemostatic, hypotensive, hepatotropic, vasotropic, cardiant, haemostatic, hypotensive, hepatotropic, immunosuppressive, gynaecological, antibacterial, endocrine, immunosuppressive, gynaecological, antiparkinsonian, anticonvolsant, tranquiliser, analgesic, nephrotropic, antinfertility and antilipaemic crimquiliser, analgesic, nephrotropic, antinfertility and antilipaemic activities. The NOVX polypeptide, nucleic acid or antibody of the cativities are cardiomyopathy, atherosoclerosis, diabetes or a disorder related to cell signal processing and metabolic pathway modulation.

Contrementing diseases such as asthma, allergies, emphysema, autoimmune disease, graft-versus-host disease, arthritis, cancer, stroke, heemophilia, obesity, Alzheimer's disease and pain. The nucleic acids may be useful nof the invention which is related to human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated polypeptide disorder, e.g. cardiomyopathy, atherosclerosis, diabetes, cancer, Parkinson's disease or
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RIEGER D K.
EDINGER S R.
                                                                                                                          LI L.
CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
SHIMKETS R A. GROSSE W M. SZEKERES E S. VERNET C A M.
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SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                          GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                                                                             MILLET I.
SCIORE P.
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                                                                                                                       (LILL/)
(CASM/)
(BOLD/)
(GORM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCIO/)
(ELLE/)
(MACD/)
(SMIT/)
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(RIEG/)
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The invention relates to a method for screening genes involved in aging and/or aging-associated diseases (AAD) or in oxidative stress. The method involves mutating and cultivating a yeast cell, enriching the population for mother cells, labelling the mother cells and isolating the highly labelled cells. The present sequence is human APOA1 protein. This sequence is used to illustrate the method of the invention
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181 DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening genes involved in aging and/or aging-associated diseases or in oxidative stress by mutating and cultivating a yeast cell, enriching the population, labeling the mother cells and isolating the highly labeled cells.
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                                                                                                                                                                                                                                                                                                               stress; AAD; APOA1.
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100.0%; Pred. No. 3.2e-99;
iive 0; Mismatches 0;
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                                      GLLPVLESFKVSFLSALEEYTKKLNTQ
                                                                        241 GLLPVLESFKVSFLSALEEYTKKLNTQ
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                                                                                                                                                                  standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding an inhibitor of a pro-atherogenic molecule operationally linked to a macrophage-specific expression element, useful for reducing or inhibiting atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                     Pro-atherogenic; atherosclerosis; therapy; human; apolipoprotein; APOAl; macrophage-specific expression element.
                                        DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
                   DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a nucleic acid comprising a nucleotide sequence encoding an inhibitor of a pro-atherogenic molecule operationally linked to a macrophage-specific expression element. The invention is useful for reducing and inhibiting atherosclerosis. The present sequence is human apolipoprotein (APOAI) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKAAVLTLAVLPLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGKOLNIKILDNWDSVTSTFSKIREQIGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOPYLDDFOKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VOPYLDDFOKKWOEEMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMRDRARAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1362; DB 8;
100.0%; Pred. No. 3e-99;
iive 0; Mismatches 0;
                                                                                         267
                                                                                                                            267
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                                                                                                                      GLLPVLESFKVSFLSALEEYTKKLNTQ
                                                                                       GLLPVLESFKVSFLSALEEYTKKLNTO
                                                                                                                                                                                                                       Ŕ
                                                                                                                                                                                                                       standard; protein; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2002; 2002US-00186288.
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                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-061641/06.
N-PSDB; ADI19751.
                                                                                                                                                                                                                                                                                                                                 Human APOAl protein.
                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DAVI/) DAVIS R A.
                                                                                                                                                                                                                                                                                                                                                                   Pro-atherogenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                              22-APR-2004
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180 188

249 GLLPVLESFKVSFLSALEEYTKKLNTQ 275

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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRR) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                       Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                  SeqID253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
99.8%; Score 1359; DB 7; Length 267;
Best Local Similarity 99.6%; Pred. No. 5.3e-99;
Matches 266; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                         human; screening assay; diabetes mellitus;
                                                                                                                Human heat mitochondrial protein as a therapeutic target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 253; 180pp; English.
¥.
ADJ68447 standard; protein; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2003; 2003WO-US010870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BUCK-) BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-845369/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                  WO2003087768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOKOR
                                                                                                                                                         mitochondrial;
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                          06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ghosh SS, 1
Warnock DE;
                                      ADJ68447;
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1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS

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ALGKOLNIKLIDDWDSVTSTFSKLREOLGPVTQEFWDNLEKETEGLROEMSKDLEEVKAK 120
                                                     61 ALGKQLNLKILIDNWDSVTSTFSKIRRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                      VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                      180
                                                                                                                                                                         DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO 240
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                                                                                                                          121 VQPYLDDFQKKWQEEMELYRQKVDPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV
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1 MKAAVLTLAVLFLTGSQARH.....SFKVSFLSALBEYTKKLNTQ 267
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 2, Appli	Sequence 15, Appl	Sequence 30, Appl	Sequence 75, Appl	Sequence 260, App	Sequence 30, Appl	Sequence 10, Appl	Sequence 219, App	Sequence 226, App	Sequence 74, Appl	Sequence 253, App	Sequence 27, Appl	Sequence 16, Appl
SUMMARIES		QI	US-09-803-918A-2	US-09-987-107-15	US-09-802-640-30	US-10-032-189-75	US-10-283-599-260	US-10-403-902A-30	US-10-186-288-10	US-10-038-854-219	US-10-038-854-226	US-10-032-189-74	US-10-408-765A-253	US-09-919-039-27	US-09-987-107-16
		DB	σ	0	10	14	14	14	15	15	15	14	16	10	6
	Query	Length	267	267	267	267	267	267	267	267	267	267	267	267	267
	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.8	8.66	98.8	95.9
		Score	1362	1362	1362	1362	1362	1362	1362	1362	1362	1359	1359	1346	1306
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Sequence 77, Appl Sequence 223, App Sequence 230, Appl Sequence 76, Appl Sequence 220, Appl Sequence 220, Appl Sequence 27, Appl Sequence 27, Appl Sequence 8, Appli Sequence 60, Appl Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 54, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 24, Appl Sequence 22, Appl	equence 52, Al equence 44, Al equence 62, Al equence 64, Al
4 US-10-032-189 5 US-10-038-854 6 US-10-038-854 7 US-10-038-854 8 US-09-987-107-107-108-09-987-107-107-108-09-987-107-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-107-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-108-09-987-1087-1087-1087-1087-108-09-987-1087-1087-1087-1087-1087-1087-1087-10	-09-987-107- -09-987-107- -09-987-107-
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1306 1306 1306 1229 1229 1229 1229 1229 1229 1229 122	1241 1241 1238 1235
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 2 E 4 4 3

## ALIGNMENTS

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REBUILT 1 Sequence 2, Application US/09803918A Sequence 2, Application US/09803918A Sequence 2, Application US/09803918A Sequence 2, Application US/09803918A Sequence 2, Application US/0980318A GENERAL INFORMATION: APPLICANT: Burger, Danielle APPLICANT: Rohno, Tadahiko APPLICANT: Rohno, Tadahiko APPLICANT: Rohno, Tadahiko APPLICANT: Rohno, Tadahiko TITLE OF INVENTION: APO-A-1 REGULATION OF T-CELL SIGNALING FILE REFERENCE: 2003-3035-0000 FILE REFERENCE: 2001-07-19 CURRENT APPLICATION NUMBER: 60/199,008 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR PELICATION NUMBER: 60/193,551 PRIOR FILING DATE: 2000-03-31 SOFTWARE: PATENTIN VOY: 2.1 SEQ ID NO 2 LENGTH: 267 TYPE: PRT CORGANISM: Homo sapiens US-09-803-918A-2	Query Match 100.0%; Score 1362; DB 9; Length 267; Best Local Similarity 100.0%; Pred. No. 1.2e-92; Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps	Qy 1 MKAAVITLAVLFITGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	QY         6.1 ALGKQLNLKLI.DNWDSVTSTFSKI.REQLGPVTQEFWDNLEKETEGI.RQEMSKDLEBVKAK           DD         6.1 ALGKQLNLKLI.DNWDSVTSTFSKI.REQLGPVTQEFWDNLEKETEGIRQEMSKDLEBVKAK

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Gaps

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61 ALGKQLNIKLIDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ALGKOLNIKILDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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                                                                                                                                                                                                                                                                                                                                                              1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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APPLICANT: MacDougall, John R
APPLICANT: Mathson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
                                                                                                                                                                                                                                                                                                                   0; Indels
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE FILE REPREBRICE: 24.36-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARR: FREUSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 30
LENGTH: 267
                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                       Score 1362; DB 10
Pred. No. 1.2e-92;
                                                                                                                                                                                                                                                100.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 75, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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Linda
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Patturajan, Meera
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gunther, Erik
Millet, Isabelle
Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gangolli, Esha A
                                                                                                                                                                                                                                                                                                                   Matches 267; Conservative
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                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Gorman,
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                    121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELGEKLSFLGEEMFDRARAHV 180
                                                                                                                                           DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
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                           VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV
                                                                                                                  DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO
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Publication No. US20030036057A1
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Braun, Andreas
APPLICANT: Kleyn Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1362; DB 9;
; Pred. No. 1.2e-92;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, JONAS
TITLE OF INVENTION: APOLIDOPROTEINS ANALOGUES
FILE REPREBACE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                     241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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Best Local Similarity 100.0%;
Matches 267; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-802-640-30
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LENGTH: 267
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61 ALGKQLNIKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKAAVLILAVLFLIGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-403-902A-30

Sequence 30, Application US/10403902A

Publication No. US20030224418A1

SERENAL INFORMATION:

APPLICANT: Braun, Andreas

APPLICANT: RISH, Aruna

TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE

FILE REFERENCE: 24736-2048B

CURRENT PAPLICATION NUMBER: US/10/403,902A

CURRENT PILING DATE: 2003-07-21

FRIOR APPLICATION NUMBER: 09/802,640
                                                                                                                                                                                                                                                                                                            FILENG APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTTAIL ABOUTER A
REGISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 009196-0007-999
TELEPHONE: 650-493-5556
TELEPAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 260
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 267, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                        COMPUTER READABLE FORM:
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                                                                             10036-2811
  New York
                                                       USA
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                                                       COUNTRY:
ZIP: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VQPYLDDFQKKWQEEMELYRQKVEPLRABLQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
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APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Butterer, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
TITLE OF SEQUENCES: 274
CORRESPONDENCE: 274
ADDRESS:
ADDRESS:
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100.0%; Score 1362; DB 14; Length 267;

Best Local Similarity 100.0%; Pred. No. 1.2e-92;

Matches 267; Conservative 0; Mismatches 0; Indels 0;
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STREET: 1155 Avenue of the Americas
             PRIOR PLING DATE: 2000-12-21
PRIOR PLING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/259, 435
PRIOR APPLICATION NUMBER: 60/269, 171
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-22
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279, 840
PRIOR PILING DATE: 2001-03-39
PRIOR PILING DATE: 2001-03-39
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/309, 247
PRIOR PILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/309, 247
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-08-17
NUMBER OF SEQ 1D NOS: 260
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Publication No. US20030208059A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/257,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-032-189-75
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LENGTH: 267
TYPE: PRT
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181 DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
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APPLICANT: MACDOUGAIL, JOHN R
ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
ITILE OP INVENTION: Proteins and Nucleic Acids Encoding Same
ITILE OP INVENTION: Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: 60/258,928
FRIOR PELING DATE: 2000-10-22
FRIOR APPLICATION NUMBER: 60/259,415
FRIOR APPLICATION NUMBER: 60/259,785
FRIOR APPLICATION NUMBER: 60/259,785
FRIOR APPLICATION NUMBER: 60/259,832
FRIOR APPLICATION NUMBER: 60/279,832
FRIOR APPLICATION NUMBER: 60/279,832
FRIOR APPLICATION NUMBER: 60/279,833
FRIOR APPLICATION NUMBER: 60/289,893
FRIOR APPLICATION NUMBER: 60/289,893
FRIOR PILING DATE: 2001-04-13
FRIOR PILING DATE: 2001-04-13
FRIOR FILING DATE: 2001-04-13
FRIOR FILING DATE: 2001-04-25
FRIOR APPLICATION NUMBER: 60/286,683
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                                                        241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                           241 GLLPVLESFKVSFLSALEEYTKKLNTO
                                                                                                                                                                                                                                       ; Sequence 219, Application US/10038854; Publication No. US20040022781A1; PEDELGALION: PROFEMATION: APPLICANT: Spytek, Kimberly A
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Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Burgess, Catherine B
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
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Millet, Isabelle
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Wolenc, Adam R
Vernet, Corine
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Rastelli, Luca
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Sequence 10, Application US/10186288

Publication No. US20040001810A1

GENERAL INFORMATION:
APPLICANT: Davis, Roger A.

TITLE OF INVENTION: Compositions and Methods for Treating;
TITLE OF INVENTION: Atheroscierosis
FILE REFERENCE: P-RD 5299

CURRENT APPLICATION NUMBER: US/10/186,288

CURRENT FILING DATE: 2002-06-26

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 267; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                     Query Match 100.0%; Score 1362; Best Local Similarity 100.0%; Pred. No. 1... Matches 267; Conservative 0; Mismatches
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                          NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 267
PRIOR FILING DATE: 2001-03-09
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ORGANISM: Homo sapiens
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61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2001-04-25
REGARDING DATE: 2001-04-25
REGARDING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                  100.0%; Score 1362; DB 15; Length 267; 100.0%; Pred. No. 1.2e-92; vative 0; Mismatches 0; Indels 0;
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkers, Richard A
Grosse, William M
Szekeres, Edward S
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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MacDougall, John R
Smithson, Glennda
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Gorman, Linda
Gorman, Linda
Gangolli, Esha A
Fernandes, Blma R
Rieger, Daniel K
Galinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
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Best Local Similarity 100.
Matches 267; Conservative
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                                                                                                                                            61 ALGKOLNIKALLDNWDSVTSTFSKLREOLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                         VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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                                                                                                                                                                                                                                                                                                                               DALRITHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
                                                                                    1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                                                              1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
                          Gaps
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                        Indels
      100.0%; Pred. No. 1.2e-92; ative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/038,854

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: 60/258,928

PRIOR PILING DATE: 2000-12-29

PRIOR PILING DATE: 2001-01-2

PRIOR PILING DATE: 2001-01-02

PRIOR PILING DATE: 2001-01-02

PRIOR PILING DATE: 2001-01-04

PRIOR PILING DATE: 2001-01-04

PRIOR PILING DATE: 2001-01-04

PRIOR APPLICATION NUMBER: 60/259,185

PRIOR APPLICATION NUMBER: 60/279,833

PRIOR APPLICATION NUMBER: 60/279,833
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Publication No. US20040022781A1
GENERAL INFORMATION:
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Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li, Li
Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
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Millet, Isabelle
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Gusev, Vladimir Y
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Gunther, Brik
    Best Local Similarity 100.
Matches 267; Conservative
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TITLE OF INVESTIGATION GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-003 US CURRENT APPLICATION NUMBER: US/09/919,039 CURRENT APPLICATION NUMBER: 60/222,113 PRIOR FILING DATE: 2000-07-28 NUMBER OF SEQ ID NOS: 401 SOFTWARE: PERL PROGRAM
SEQ ID NO 27
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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OTHER INFORMATION: Incyte ID No. US20030108871A1 2516070CD1
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FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 253
LENGTH: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 27, Application US/09919039; Publication No. US20030108871A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6%;
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 264; Conservative
                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-408-765A-253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-09-919-039-27
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                                                                                                                                                                                       TYPE: PRT
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APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dalle B.
IITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
     INVENTION: Proteins and Nucleic Acids Encoding Same
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Pred. No. 1.9e-92;
1; Mismatches 0;
                  THILE REFERENCE: 21402-228

CURRENT APPLICATION NUMBER: US/10/032,189

CURRENT PILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/259,17495

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-22-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-29

PRIOR FILING DATE: 2001-03-29

PRIOR FILING DATE: 2001-03-29

PRIOR FILING DATE: 2001-03-29

PRIOR FILING DATE: 2001-03-19

PRIOR FILING DATE: 2001-04-11

PRIOR FILING DATE: 2001-04-11

PRIOR FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 60/283,656

PRIOR FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 60/309,247

PRIOR APPLICATION NUMBER: 60/309,247

PRIOR APPLICATION NUMBER: 60/311,754

PRIOR APPLICATION NUMBER: 60/311,754

PRIOR APPLICATION NUMBER: 60/313,331

PRIOR PILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 60/313,331

PRIOR PILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 60/313,331
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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Best Local Similarity 99.6
Matches 266, Conservative
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US-10-408-765A-253
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61 ALGKQLNLKLLDNWDSVTSTVSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sciore, Faul
APPLICANT: Sciore, Faul
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: Sciore, Science
TITLE OF INVENTION: Percteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,71
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-08-17
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                            Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
                                                                                                                                 Vernet, Corine A.M
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US-10-032-189-77
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Gorman, Linda
Gangolli, Esha R
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
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Best Local Similarity 95.1
Matches 254; Conservative
                                                                                                                                                                                          Stacie
                                                                                                                                                                   Li, Li
Casman, S
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APPLICANT:
APPLICANT:
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121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ALGKQLNLKLLDNWDSVTSTVSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
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                                                                                   DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKATVLTLAVLPLIGSQARHFWQQDEPPQTPWDRVKDLVTVYVBALKDSGKDYVSQFEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO
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95.9%; Score 1306; DB 9; Length 267;
Best Local Similarity 95.1%; Pred. No. 1.6e-88;
Matches 254; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN
APPLICANT: GRAVERSEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
FRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
FRIOR APPLICATION NUMBER: DK PA2001 00057
FRIOR APPLICATION NUMBER: DK PA2001 01682
FRIOR FILING DATE: 2001-01-15
FRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 16
LENGTH: 267
                                                                                                                                                                                             241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
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Sequence 77, Application US/10032189

Sequence 77, Application US/10032189

Publication No. US20030170630A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P

APPLICANT: Tchernev, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Zerhusen, Bryan D

APPLICANT: Patturajan, Meera

APPLICANT: Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Macaca fascicularis
US-09-987-107-16
                                                      181
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APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proceins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proceins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/259,928
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259,814
PRIOR PLING DATE: 2001-02-20
PRIOR PLING DATE: 2001-02-20
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-04-3
PRIOR PLING DATE: 2001-04-3
PRIOR PLING DATE: 2001-04-25
PRIOR PRIOR PLING DATE: 2001-04-25
PRIOR PLING DATE: 2001
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                        241 GLLPVLESFKVSFLSALEEYTKKLSTQ 267
241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
                                                                                                                                                          US-10-038-854-223
; Sequence 223, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        Li, Li
Wolenc, Adam R
Vernet, Corine
Bisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenoy, Suresh G
Rastelli, Luca
Camman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
Smithson, Glennda
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gorman, Linda
Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guo, Xiaojia S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                         61 ALGKOLNIKALDNWDSVTSTVSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
                                                                                                                                             VQPYLDDFQKKWQEEMELYRQKVEFLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
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                                           1 MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
  Gaps
  .;
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7; Indels
  Mismatches
                                                                                                                                                                                                                                                                             241 GLLPVLESFKVSFLSALEEYTKKLSTQ 267
                                                                                                                                                                                                                                                              241 GLIPVLESFKVSFLSALEEYTKKLNTQ 267
  9
  254; Conservative
                                                                                                                                              121
    Matches
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Search completed: December 21, 2004, 07:30:10 Job time : 133.2 secs

Tue

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

December 21, 2004, 10:45:04; Search time 16 Seconds (without alignments) 1022.303 Million cell updates/sec Run on:

US-09-803-918A-2_COPY_25_194 885 1 DEPPQSPWDRVKDLATVYVD......RARAHVDALRTHLAPYSDEL 170 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

seq length: 0 seq length: 170 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apolipoprotein A-I	apolipoprotein AI	apolipoprotein A-I	apolipoprotein A-I	conserved hypothet	hypothetical prote	conserved hypothet	conserved hypothet		ski-related protei	tropomyosin TPM2 -	hypothetical prote	hypothetical prote			⋾	trichohyalin compo	hypothetical prote	hypothetical prote	light meromyosin -	plasminogen-bindin	hypothetical prote		gas-vesicle protei	conserved hypothet	hypothetical prote	translocation prot	flagella-related p	
SUMMARIES		S21830	S67972	A56866	A05313	B69818	T23249	G90201	C95164	B98030	B46598	S48396	F75559	S74746	T12720	A97836	F64117	C64576	A84228	S66805	150496	S70457	T05610	G86722	B27475	A83265	AD1568	H83434	H75062	G72208
	DB		~	~	~	7	~	~	7	~	7	~	~	~	N	~	~	~	~	~	~	N	~	N	N	~	~	~	7	7
	ngth	164	34	36	20	118	164	146	129	129	66	191	163	135	154	159	129	141	123	113	142	147	148	79	162	109	118	158	160	140
J	Query Match	41.8	12.0	12.0	11.4	11.1	10.2	10.2	9.9	9.9	9.8	9.6	9.3	9.0	8.9	8.9	8.9	8.9	æ	8.7	8.7	8.7		9.8			9.8	9.8	9.8	8.5
	Score	ī	106	106	101	98	90.5	90	88	æ	86.5	82	82.5	79.5	79	79		78.5	78	77	77	77	77	•	76.5	97	16	9/	96	75.5
	Result No.		8	m	4	2	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	hypothetical prote	hypothetical prote	hypothetical prote	unknown protein en	conserved hypothet	kinetoplastid memb	hypothetical prote	hypothetical coile	troponin C (Ca(2+)	hypothetical prote	hypothetical prote	antifreeze protein	hypothetical prote	hypothetical prote	neurofilament trip
B24733	T29401	C91001	A83960	D85846	F72296	553443	H69881	T38886	A53051	D64431	H96567	A59010	H71194	T33585	C22702
0	~	7	7	~	~	N	7	7	~	~	~	N	N	~	7
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114	146	133	138	143	170	79	167	137	152	163	169	108	108	133	142
										8.3 163					
8.5	œ v.	8.4		8.4	8.4	8.4	8.4	8.3	8.3		8.3	8.2		8.2	8.2

## ALIGNMENTS

RESULT 1

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apolipoprotein A-I - pig (fragment)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Accession: S21830
R.Trieu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
R.Trieu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
R.Trieu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
A.; Reference number: S21830
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A.; Reference number: S21830
A.; Residues: 1-164 < TRI>
A.; Residues: 1-164 < TRIPAIN: TRIPAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 370; DB 2; Length 164; 79.8%; Pred. No. 8.5e-17; Live 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 79.8
Matches 71; Conservative
S21830
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## 63 4 LRQEMSKDLEEVKKKVQPYLDDFQNKWQEEMETYRQKWAPLGAEFREGARQKVQELQEKL 142 SPLGEEMRDRARAHVDALRTHLAPYSDEL 170 64 SPI. BERI. BSRI. BAHVRAI. BOHVA PYSDDI. 92 셤 ઠે ò Ę

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Gaps

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RESULT 2 S67972	
apolipoprotein AI - goose (fragment) C;Species: Anser anser (domestic goose)	e)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C:Accession: S67972	n 13-Mar-1997 #text_change 09-Jul-2004
R;Hermier, D.; Sellier, N.; Rousselot-Pailley, D.; Forgez, P. Birr J Biorham 234 586-591 1995	-Pailley, D.; Forgez, P.
A, Title: Characterization of apolipoproteir	A;Title: Characterization of apolipoproteins B-100, AI and C from plasma lipoprotein in

ö Gaps ö Query Match 12.0%; Score 106; DB 2; Length 34; Best Local Similarity 54.5%; Pred. No. 0.61; Matches 18; Conservative 9; Mismatches 6; Indels A; Reference number: 867972; MUID:96128192; PMID:8536707 A; A; Scession: 867972; MUID:96128192; PMID:8536707 A; Status: preliminary A; Molecule type: protein A; Residues: 1-34 <HER.>
A; Cross-references: UNIPROT:Q9PRR6 C; Superfamily: apolipoprotein A-I

```
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadae, Y.; Sato, T. Saronlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serorakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, A; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Yasumoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Athors: Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchlyama, A; P.; Complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A, Accession: B69818
A, Status: preliminary: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:09XUV5; EMBL:281560; PIDN:CAB04544.1; GSPDB:GN00023; CESP:K0*
A;Experimental source: clone K02E2
                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-118 «KUN»
A;Cross-references: UNIPROT:007516; GB:299109; GB:AL009126; NID:92633260; PIDN:CAB12840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPELQPISPPSIHD-------DLINDMDGGMFGSEKTDDSSLEDLQLHVQEM 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein K02E2.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GKQLREKMKTNYDSFEETIKRLKS------DGLALKDQLIKAAKESTDVIKDVGGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKOLNLKLLDNWDSVTSTFSKLREOLGPVTOEFWDNLEKETEGLR--QEMSKDLEEVKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 98; DB 2; Length 118; larity 27.5%; Pred. No. 7.6; Conservative 25; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.2%; Score 90.5; DB 2; 22.7%; Pred. No. 32; ive 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19716
A;Accession: T23249
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental gource: gtrain 168 C, Genetics:
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Best Local Similarity
Matches 40; Conserv
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A; Introns: 35/1; 62/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Gene: CESP: K02E2.7
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C; Species: Errthrocebus patas (red guenon, hussar)
C; Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C; Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C; Date: 05-Jun-1987 #sequence_revision 05-Jun-1987
B; Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
B; Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus A; Recession: A0313
A; Accession: A0313
A; Accession: A0313
A; Residues: 1-20 cMAH-
A; Rossidues: 1-20 cMAH-
A; Cross-references: UNIPROT:P18647
C; Superfamily: apolipoprotein A-I
C; Keywords: Cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Bacillus subtiles
C;Species: Bacillus subtiles
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B68918
C;Accession: B68918
C;Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Coulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
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                                                                                                                                                                                                                                apolipoprotein A-I - Japanese quail (fragment)
C'Species: Coturnix coturnix japonica (Japanese quail)
C'Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: As6866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternate names: apo-A-I
Species: Erythrocebus patas (red guenon, hussar)
Bate: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004;
Accession: A05313
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A,Note: sequence extracted from NCBI backbone (NCBIP:128831)
A,Note: this protein was found primarily as a 26K apoprotein C, Superfamily: apolipoprotein A-I
                                                                                                                                                                                                                                                                                                                        C)Accession: A56866
R)Oku, H.; Ishikawa, M.; Nagata, J.; Toda, T.; Chinen, I. Blochim. Blophys. Acta 1167, 22-28, 1993
A;Title: Lipoprotein and apoprotein profile of Japanese qua; Reference number: A56866; MUD:93213845; PMID:8461329
A;Accession: A56866
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-36 <OKU>
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                                             10; Mismatches
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Matches 18; Conservative
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; P. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I. J. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R., A;Atches Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8DPA5; GB:AE007317; PIDN:AAL00071.1; PID:g15458907; GSPDB:CC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 QLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPY 100
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NiAlternate names: protein YIL138c
C.Species: Saccharomyces cerevisiae
C.Species: Q2-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ski-related protein SnoN - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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J. Biol. Chem. 268, 13710-13716, 1993
A;Title: Complex formation between proteins encoded by the ski gene family.
A;Reference number: A46598; MUID:93293901; PMID:8514802
A;Accession: B46598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 129;
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LDHAEADRQELQDELRQERE-----ARQKLEMMIKEL 96
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.9%; Scoll 25.8%; Pred. No. 30,
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C, Keywords: DNA binding; tandem repeat
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A; Residues: 1-56;57-99 <NAG>
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R;Churcher, C.
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les 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9UMV7; GB:AE006641; NID:g13813718; PIDN:AAK40870.1; GSPDB:G
C;Genetics:
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                                                      Chan-
         Rishe, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

Abanalak, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: G90201
A; Accession: G90201
A; Residues; preliminary
A; Malesidues: 1-146 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEP 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 10.2%; Score 90; DB 2; Local Similarity 22.4%; Pred. No. 30; nes 33; Conservative 34; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Matches
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A; Accession: S74746
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: O: Eisen, U.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
N.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F7559
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 cWHL>
A;Cross-references: UNIPROT:Q9RY46; GB:AE001873; GB:AE000513; NID:g6457764; PIDN:AAF0970
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
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       GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763208;
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A;Cross-references: UNIPROT:P40414; GB:Z47047; EMBL:Z38059; NID:g603997 R;Drees, B.; Brown, C.; Barrell, B.G.; Bretscher, A.
J. Cell Biol. 128, 383-392, 1995
A;Title: Tropomyosin is essential in yeast, yet the TPM1 and TPM2 produ A;Reference number: A56490; MUID:95146545; PMID:7844152
A;Recession: A56490
A;Status: pretilminary; nucleic acid sequence not shown A;Residues: 1-161 <DRE>
A;Cessereferences: GB:Z47047; GB:Z38059; NID:g603997; PID:g763208
C;Genetics: A;Gene: SGD:S0001400; MIPS:YILL38C
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hypothetical protein slr0978 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
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70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 85; DB 22.7%; Pred. No. 70; iive 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                    A;Map position: 9L
C;Superfamily: tropomyosin TPM1
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.7%
Matches 29; Conservative
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S;4446
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Rosidues: 1-13 cKAN-
A;Rosidues: 1-13 cKAN-
A;Cross-references: UNIRROT:P72881; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1689
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A;Residues: 1-154 <PFI>
A;Rorss-references: UNIPROT:080194; EMBL:AF065411; NID:32249585; PID:33249589; PIDN:AAC2
A;Experimental source: host Methanobacterium thermoautotrophium strain Marburg
C;Superfamily: Methanobacterium phage psiM2 hypothetical protein 4
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C; Species: Rickettsia conorii
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: A97836
R; Ogata, H; Audic, S:; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A; Reference number: A97700; MUID:21442074; PMID:11557893
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C,Superfamily: Synechocystis hypothetical protein slr0489
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8.9%; Score 79; DB 2;
Best Local Similarity 26.1%; Pred. No. 1.6e+02;
Matches 31; Conservative 30; Mismatches 40
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Accession: A97816
A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-159 «KUR»
A;Residues: 1-159 «KUR»
C;Genetics:
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8.9%; Score 79; DB 2; Length 159;
Best Local Similarity 24.4%; Pred. No. 1.6e+02;
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MEDILINE-96062440; PubMed=7488287;
Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
Selection of a gene for apolitopycotein Al using autoantibodies from patient with systemic lupus erythematosus.";
Arthrits Rheum. 38.1655-1659(1995).
EMBL; S80442; AAB35539.1;
InterPro; IPR009074; Apolipo_A_E_C3.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Apolipoprotein Al homolog protein (Fragment).
Name=apolipoprotein Al homolog;
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02-MRR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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A ROBELINE=99098454; PubMed=9883985;
A ROBERTSON J.A., Bhattacharyya S., Ing N.H.;
A Robertson J.A., Bhattacharyya S., Ing N.H.;
AT "Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and receptor-alpha, c-fos and receptor-alpha, c-fos and receptor-alpha, c.fos and receptor-alpha, provine endometrium.";
A Steroid Blochem. Mol. Biol. 67:285-292(1998).

R GO; GO:0008299; F:lipid binding; IEA.
BR GO; GO:0008299; F:lipid transport; IEA.
BR GO; GO:0008299; F:lipid transport; IEA.
BR GO; GO:00042157; P:lipoprotein metabolism; IEA.
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Merrill J.T., Rivkin B., Shen C., Lahita R.G.;
"Selection of a gene for apolipoprotein Al using autoantibodies from patient with systemic lupus erythematosus.";
Arthritis Rheum. 38.1655-1659 (1995).
EMBL; S80442; AAB35539.1; -.
                                                                                                                                                                                                                                           0; Gaps
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                        Length 79;
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                                                                                                                                                                                     36.2%; Score 320; DB 2; Length 79 76.9%; Pred. No. 3.9e-13; Live 10; Mismatches 8; Indels
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56 56
56 AA; 6617 MW; 2AB38E08F1E8F1BC CRC64;
                                                                                                                    NON TER 1 1 1
SEQUENCE 79 AA; 9583 MW; 33CA72DA854A150A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 247; DB 2;
Pred. No. 1e-08;
3; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                130 AROKLHELQEKLSPLGEE 147
                                                                                                                                                                                                                                                                                                                                                                                                        Apolipoprotein Al (Fragment).
Ovis aries (Sheep).
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1 Similarity 82.1%;
46; Conservative
                                                                                                                                                                                   Query Match 36.2%
Best Local Similarity 76.9%
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9940;
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SEQUENCE
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MEDIATES 921632; PubMed=10198255;

MEDIATES 921632; PubMed=10198255;

Hamidi A81 K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;

Hamidi A81 K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;

Hamidi A81 K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;

Hamidi A81 K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;

Tardiac and cutaneous amyloidosis.;

Ediation Biophys. Res. Commun. 257:584-588 (1999).

Res Go, Go:0005576; C:extracellular; IEA.

Res Go; Go:0008289; F:lipid binding; IEA.

Res Go; Go:0008689; P:lipid transport; IEA.

Res Go; Go:0008289; P:lipid transport; IEA.

Res Go; Go:00142157; P:lipid-transportein.

Res Go; Go:00142157; P:lipid-transportein.
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                                                                                                                                                                                                       Winteroe A.K., Fredholm M., Davies W.; "Evaluation and characterization of a porcine small intestine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hōmo Bapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 217; DB 2; Length 82;
Pred. No. 1.2e-06;
5; Mismatches 12; Indels
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprocein.
NON TER 82 82
SEQÜENCE 82 AA, 9168 MW; 24625C65CBFFEDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 67
67 AA; 7433 MW; 525E1FEB7BDD5AFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                   library.";

Mamm. Genome 7:509-517(1996).

EMBL; F14868; CAA232981. -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0008289; F:lipid binding; IEA.

GO; GO:00042157; P:lippid transport; IEA.

GO; GO:0042157; P:lippid transporti IEA.

InterPro; IPR000074; Apolipoprotein.

InterPro; IPR009074; Apolipoprotein.

Pfem; PF01442; Apolipoprotein; 1.
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                                                                                                                                   TISSUE=Small intestine;
MEDLINE=96327607; PubMed=8672129;
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Matches 41, Conservative
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Les 30; Conservative
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SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
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01-MAY-2000 (
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruar A.,
Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniauw N., Joyet P., Rachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potler S., Richard G.F., Straub M.L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
"Genome evolution in yeasts.",
                                                                                                                                                                                          MEDLINE=91169902; PubMed=1909888; Akerlof E., Jornvall H., Slotte H., Pousette A.; "Identification of apolipoprotein A1 and immunoglobulin as components of a serum complex that mediates activation of human sperm motility.";
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sperm activating protein subunit I, apolipoprotein A1, SPAP subunit I
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.9%; Score 141; DB 2; Length 26; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 26; Conservative 0; Mismatches 0; Indels
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CAGL0J054349 Candida glabrata 3 end (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                             26 AA; 2930 MW; 64921A333E768D27 CRC64;
                                                                                                                                                                                                                                                 Biochemistry 30:8986-8990(1991).
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008289; F:lipid binding; IEA.
GO; GO:0008689; F:lipid transport; IEA.
GO; GO:0042157; P:lipoprotein metabolism; IEA.
InterPro; IPR000074; Apolipoprotein.
               26 AA.
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Kluyveromyces lactis (Yeast).
               PRELIMINARY;
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                                                                                                            Homo sapiens (Human)
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STRAIN=NRRL Y-1140;
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86 MS--KDLEEVKAKVQPYLDDFQKKWQ---EEMELYRQKVEPLRAELQEGARQKLHELQEK 140
                                                                                                                                                                                                                                                                                                                                                            88 ------KDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 GKSNFDNDDLKERLKDLSDEKQKIQEELENKQKDYQLAVDGHANTVKRHEAEI-----AK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GAGLASÓTEVKAAEDHWRVENARNQVLGRSTVTAPAHFWENQRREIEKLKGEIDOLKLLL 72
                                                                                                                                                                                                                                                                   40 KQLNLKL-LDNWDSVTSTFSKLREQLGPVTQEFWDN------LEKETEGLRQE
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                                                                                                                                                                                         Gaps
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                                                                                                                                                                                       27; Mismatches 47; Indels
Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382125; CAG99846.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030010; BAA82521.1; -.
                                                                     NON_TER 1 1
SEQUENCE 155 Aa; 18171 MW; 3E9137FD16A4E39A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 AA; 16803 MW; ESSE41B26F8EFE19 CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
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Last annotation update)
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                                                                                                                                          12.8%; Score 113; 1
30.5%; Pred. No. 8;
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                                                                                                                                                                                         43; Conservative
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Name=emm;
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143 AA.

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STANDARD;
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05-JUL-2004
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APHAV
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Q28502;
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                                                                                                                                                                                                                                       35 GSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMS-----
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A Hermier D., Sellier N., Rousselot-Pailley D., Forgez P.;
Hermier D., Sellier N., Rousselot-Pailley D., Forgez P.;
The Aracterization of apolipoproteins B-100, Al and C from plasma
T ipoprotein in the Goose, Anner anner. Evidence for a genetic
T polymorphism in ApoC-like apolipoproteins.";
L Bur. J. Blochem. 234:586-591(1995).
R GO; GO:0008289; F:lipid binding; IEA.
GO; GO:0008289; F:lipid binding; IEA.
GO; GO:0008869; P:lipid transport; IEA.
GO; GO:0008699; P:lipid transport; IEA.
GO; GO:0004157; P:lipid transport; IEA.
R GO; GO:0004157; P:lipid transport; IEA.
R FOR GO:0004187; Apolipoprotein.
R InterPro; IPR000074; Apolipoprotein.
R Pfam; PF01442; Apolipoprotein.
R Pfam; PF01442; Apolipoprotein.
R Pfam; PF01442; Apolipoprotein.
R Pfam; PF01442; Apolipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anser anser (domestic goose).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Anseriformes, Anatidae, Anser.
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                                                                                                                                                                            Length 138;
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            Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                    Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF128960; AAD28609.1; -
                                                                                                                                                    15656 MW; A50AE51B14EAAE1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                 54;
                                                                                                                                                                            DB 2;
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                                                                                                                                                                         Query Match 12.5%; Score 110.5; Di
Best Local Similarity 25.6%; Pred. No. 10;
Matches 34; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       34 AA
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126 DEIIKKQSETAEE 138
                                                                                                                                                                                                                                                                                                                      135 HELQEKLSPLGEE 147
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                                                                                                                                                    138 AA;
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Matches 18; Conserv
                                                                    SEQUENCE FROM N.A.
                                            NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8843;
                                                                                 STRAIN=4973;
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SEQUENCE
                                                                                           Beall B.;
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RESULT 11 LEA1_APHAV

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
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29-MAR-2004 (Rel. 43, Last amnotation update)
Late embryogenesis abundan protein 1 (Aavlea1).
Aphelenchus avenae (Mycophagous nematode).
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Aphelenchoidae; Aphelenchus.
NCBI_TAXID=70226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDF
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MEDLINE=96225955; PubMed=8635577;
MOTELIL L., Wel L., Amorim A., McDermid J., Abee C.R., Frangione B., Walker L.C., Levy B.,
Welker L.C., Levy B.,
"Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys: apolipoprotein E genotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                     105 OKKWOREMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMRDRA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 143;
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47 57 1.
69 79 2.
80 90 3.
91 101 4.
143 AA; 16028 MW; A41566258765BFB0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF423069; AAL18843.1; -.
InterPro; IPR004238; LEA.
Pfam; PF02987; LEA_4; 2.
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cholesterol acyltransferase (LCAT).
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Best Local Similarity
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                                                                    chylomicrons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10118;
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01-OCT-2003
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Q28995;
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                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                         and catabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
FEBS Lett. 379:132-134(1996).
-!- PUNCTION: Mediates the binding, internalization, and catabolism care proximates the binding. Internal lipoprotein particles. It can serve as a ligand for the LDL (apo B/B) receptor and for the specific apo-B receptor (chylomicron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erythrocebus patas monkey.";
Biochemistry 15:1928-1933(1976).
-!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr., "Characterization of the plasma lipoproteins and apoproteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 KVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDL receptor binding (Potential).
Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Brythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
Plasma; Repeat; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                  remnant) of hepatic tissues.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Secreted in plasma.
-!- SIMILARITY: Belongs to the apolipoprotein Al/A4/E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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01-NOV-1990 (Rel. 16, Last sequence update)
01-UUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein A-I (Apo-AI) (Fragment).
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                                                                                                                                                                                                                                                                                                           entities requires a license agreement (St or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo A E C3.
Pfam; PF01442; Apolipoprotein; 1.
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es 28; Conserv
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SEQUENCE
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P18647;
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Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Cebinae, Saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=96225955; PubMed=8635577;
Morelli L., Wei L., Amorim A., McDermid J., Abee C.R., Frangione B.,
Walker L.C., Levy E.;
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                      .
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                                                                       -1- SIMILARITY: Belongs to the apolipoprotein Al/A4/E family. PRI, A05313, A05313.
InterPro: IPRO09074, Apolipo A. E.C3.
Cholesterol metabolism, Direct protein sequencing; HDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 101; DB 2; Length 30; 67.9%; Pred. No. 8.1; cive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                              Score 101; DB 1; Length 20; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4A0103DCB6242BF3 CRC64;
                                                                                                                                                                                                                            SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95355312; PubMed=7629028; Motojima K., Goto S.; J. Biochem. 117:597-602 (1995).

J. Biochem. 117:597-602 (1995).

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0006289; F:lipid binding; IEA.

GO; GO:0006689; P:lipid transport; IEA.

GO; GO:0004157; P:lipoprotein metabolism; IEA.

InterPro: IPR000074; Apolipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 AA.
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                                                                                                                                                                                                                                                                                                                              2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PQSQWDXVXDFATVYVDAVXDSGXDYXS 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apolipoprotein E (Apo-E) (Fragment).
Name=APOE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                1 DEPPOTPWDRVKDLVTVYVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01442; Apolipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 37, Created)
(Rel. 37, Last seq
(Rel. 44, Last ann
                                                                                                                                                                                                                                                                                 11.4%;
85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apolipoprotein E (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 67.9
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                              Lipid transport; Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 SKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .----- 67
Gaps
                                                                                                                                                                                                                                                                                                                  LDL receptor binding (Potential).
Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
                                                                                                                                                                                                                                        InterPro; IPR000074; Apolipoprotein.
InterPro; IPR000074; Apolipo_A_E_C3.
Pfam; PF01442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
Plasma; Repeat; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2%; Score 99; DB 1; Length 107; 26.2%; Pred. No. 41; tive 19; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 KVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
12328 MW; FF88CED47BD18F7C CRC64;
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1es 27; Conservative
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96
>107
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55
77
99 >1
107 AA;
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Best Local S:
Matches 27
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SEQUENCE
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DOMAIN
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Search completed: December 21, 2004, 13:51:30 Job time: 190 secs

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885
1 DEPPQSPWDRVKDLATVYVD......RARAHVDALRTHLAPYSDEL 170
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 170
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Adacizis Human 18K Aac02278 Human pol Aac02278 Human pol Aac12095 Human MSP Aac12095 Human MSP Aac12095 Human pol Aac12095 Human pol Aac12095 Human pol Aac12095 Human MSP Ac10267 Novel hum Aac1066 Novel hum Aac1067 Novel hum Aac1067 Apo An pol App76131 Human MSP Ad770395 Human mSP Ad770395 Human mSP Ad770395 Human mSP Ad770395 Human mSP Ad67644 Apo AI pol App31744 Human apol Ad67447 Apolipopr Ad67442 Human apol Ad67442 Human apol Ad67442 Human apol Ad67442 Human apol Ad67443 Rat apoli Ag687431 Rat apoli Ad687431 Rat apoli Ad687431 Rat apoli Ad687431 Rat apoli
SUMMARIES	ADA61215 AA002278 AA02278 AA0228372 AA0224649 AA0130469 AA0130469 AA0130469 AA0130469 AA0130469 AA024648 AA024648 AA024648 AA020165 AAR20165
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% Query Match Length	170 166 166 168 1154 1159 1159 1150 120 120 121 121 121 121 121 121 121 12
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Score	529 529 529 529 529 529 529 529 529 529
Result No.	22222222222222222222222222222222222222

22222
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18-MAY-2000; 2000US-00577409

(HYSE-) HYSEQ INC

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The invention discloses a apolipoprotein A-I (apo-A-I) polypeptide or its related polypeptide, apo-A-I fragment T-cell activation inhibitor-like (AFTI) polypeptide, or a fragment or an allelic or splice variant. Apo-A-I and its derivatives are used in regulating T-cell-mediated activation of monocytes. Also disclosed is an antibody produced by immunising an aim a usbel or its fragment. Apo-A-I and a selective binding agent, or its fragment. Apo-A-I is useful for reducing inflammation, interleukin (IL)-lbeta secretion or treating IL-I or TNF-alpha mediated disease in a subject, or for treating IL-I or TNF-alpha mediated disease in a subject. The monocyte activation in a patient, for determining whether a compound inhibits activity or production of apo-A-I, for detecting or quantifying the amount of apo-A-I in a sample, for regulating T-cell-mediated inhibits activity or production of apo-A-I, for detecting or quantifying the amount of apo-A-I in a sample, for regulating T-cell-mediated conformed activity or production of apo-A-I, for detecting or quantifying the amount of apo-A-I in a sample, for regulating T-cell-mediated conformed diseases used and chronic IL-I-conformed diseases used as an immunogen to raise antibodies, for treating acute and chronic IL-I-conformediated diseases used as the pancreatitis, all pancreatitis, and acute as can chronic TNF-mediated diseases such as acute pancreatitis, all pancreatitis, and acute conformed activity or barkingon's disease, porionasis, uveitis, and acute conformediated diseases, pulmonary fibrosis, reperfusion injury, rheumatic diseases, septic shock, systemic lupus erythematosus and thyroiditis.

Chey applications, to test for the presente of apo-A-I, as hybridisation probes in diagnostic assays, for diagnostic applications, to test for the presence of apo-A-I, and hybridisation probes in diagnostic assays, for diagnostic applicating and in therappetures. The sequence presented is the human 18K N-Ferminal and the presented in assamble the presented in a sequence of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; architits; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 885; DB 6;
; Pred. No. 8.8e-66;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAO02278 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 16170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal apo-A-1 protein fragment
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100.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170 AA;
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141
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                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA01310) that exhibit activity elating to sytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LKDSGRDYVSQFEGCALGKQLNLKLLDNWDSETSTFSKLREQLGPVTQEFWDNLEKDTEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; of sutoimmune disorder; allergy; multiple sclerosis; rhematoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
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                                                                                                                                                                                                                              Claim 20; SEQ ID NO 16170; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.1%; Score 727; DB 4; Length 151; 94.0%; Pred. No. 1.1e-52; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secretory protein, Seq ID No 729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 SPLGEEMRDRARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU28372 standard; protein; 166 AA
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                                                                                                              2001-514838/56.
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                                                                                                                                  N-PSDB; AAI82209.
                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                        Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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131 PLRAELQEGARQKLHELQEKLSPLGEEDADRRRAHV 166

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remadeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and responsation of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, contingent disease, huntington's disease, and amyotrophic lateral solution, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, or periodontal disease. Purthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and fibracians antimed and preserver combined immunodeficiency (SCID), batterial or funcal infertions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response. AAU28020-AAU28395 represent novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid archritis, diabetes mellitus, myasthemia gravis, allargic reactions and conditions, such as asthem or other respiratory problems. In addition, (I) affects blorbythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbobydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
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                                                                                                                                                                                                                                                                  C, Wehrman T, Ren F, Ma Y, Zhou Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 647.5; DB 4; Length 166; Pred. No. 5.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 729; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequences of the invention
                                                                                                                                                                                                                                                                     Хű
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                                                                 19-MAY-2000; 2000US-00574454.
17-UIN-2000; 2000US-00596193.
14-UIL-2000; 2000US-00616847.
19-SEP-2000; 2000US-00663163.
20-OCT-2000; 2000US-00693267.
05-MAR-2001; 2001WO-US004942.
                                                2000US-00519705
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                                                                                                                                                                                                                                                               Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                         2001-589934/66.
                                                                                                                                                                                                                                                               Liu C, A
Yang Y,
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                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-589934/
N-PSDB; AAS45272.
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                                                                                                                                                                                                                                                             YT,
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Zhao
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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36311) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-telated disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
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                                                                                                                                                                                                                                                         gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.
                                                                                                                                                                                                                                       Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Pred. No. 4.4e-43;
.....rhes 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Page 402; 735pp; English.
                                                                                                                                                                            Human GENSET protein SEQ ID 171.
ABP75964 standard; protein; 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE24649 standard; protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-2001; 2001WO-IB000914.
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98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-075548/07.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200283898-A1.
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                  21-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bejanin S,
                                                          ABP75964;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a membrane scaffold protein (MSP), that self assembles in the absence of phospholipid, with a phospholipid or a mixture of phospholipid, into a nanoscale particle of 5-500 mm in diameter, in an aqueous environment, where the membrane scaffold protein diameter, in an aqueous environment, where the membrane scaffold protein is amphipathic and forms at least one alpha helix. The nanoscale particle comprising MSP is useful for identifying a competitor of binding of a ligand to a receptor protein which is incorporated within the nanoscale particle particle together with MSP, by contacting ansocale particle and a ligand to a receptor protein which a detectable ligand to produce nanoscale particle. Sound detectable ligand, contacting the bound ligand with a test compound, and measuring detectable ligand released from the particle, such that a competitor of ligand binding is identified when contacting the bound ligand results in release of the detectable ligand. The cincenton is useful for the incorporation of additional hydrophobic protein molecules. The nanoscale particle can form tags for purification and physical manipulation of disks such as entities for rapid and reproducible assay and crystallisation. The nanoscale control of particle and MSP are useful in biotechnology, pharmaceutical industries and in research areas. The nanoscale particle is useful for structure/function correlation, structure determination, bioseparation and drug discovery. The present sequence is MSPID5-6 protein
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                              Human, membrane scaffold protein; MSP; phospholipid; nanoscale particle; hydrogel; gold biosensor surface; reproducible assay; crystallisation; biotechnology; pharmaceutical industry; structure determination; bioseparation; drug discovery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE 85
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Human MSP1D5-6 (helices 5 and 6 deleted) protein.
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Best Local Similarity 74.5%; Pred. No. 3.4e-36;
Matches 108; Conservative 5; Mismatches 25
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N-PSDB; AAD39711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sligar SG,
                                                                                                                                                                                                                                                                                                    Synthetic.
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The invention relates to human polynucleotides (AAI79941-AAI91841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeries in other cell populations. The polymeries or peptide therapy. The polymeries have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing diagnosing disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 REQLGPVTQEFWDNLDKETEGLTHEMSKDLEDVNAKVQTYLYDFQKTWQKEL-TFTAESE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                 Human, cytokine; cell proliferation; cell differentiation; gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPPOSPWDRVMDLATAYVDGLKDSGRDYASQFEGYALGKQLNLMLLDNWDSVTYTFSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 25987; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for and treating e.g. leukemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%; Score 501.5; DB 4
79.5%; Pred. No. 6.6e-34;
ive 7; Mismatches 17
AAO12095 standard; protein; 154 AA.
                                                                                                              Human polypeptide SEQ ID NO 25987.
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-514838/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PL 122
                                                                                                                                                                                                                                                                                   WO200164835-A2,
                                                                                                                                                                                                                                               Homo sapiens.
                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                        07-SEP-2001.
                                     AA012095;
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used a suntitional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or AMU29510-AAMJ3304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
                                                                                             Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 476.5; DB 4; Length 120; Pred. No. 5.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%; Scur. 79.7%; Pred. No. 5... 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 DEPPQSPWDRVKDLATVYVDVLKDSGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 297; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU30267 standard; protein; 120 AA
                                                   Novel human secreted protein #960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted protein #758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                                                                                               18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
  18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611725/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 120 AA;
                                                                                                                                                                                                                                      WO200179449-A2.
                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                    25-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and simulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 NLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                     Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.2%; Score 479.5; DB 4;
89.0%; Pred. No. 3.3e-32;
ive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 297; 765pp; English.
AAU30468 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU30469 standard; protein; 120 AA.
                                                                                                                                         Novel human secreted protein #959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160
                                                                                               (first entry)
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Best Local Similarity 89.0'
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                              WO200179449-A2
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2001
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THE DESCRIPTION OF THE PRICE OF

RESULT 8 AAU30469

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New membrane scaffold protein for forming nanoscale particles, usef
biological research, self assembles with(out) phospholipids into a
nanoscale particle in an aqueous environment.
                                                                                                                                                                                                                                                                                                                            Claim 8; Page 38; 112pp; English
                                                                                                               20-NOV-2001; 2001WO-US043451
                                                                                                                                           20-NOV-2000; 2000US-0252233P
                                                                                                                                                                      (UNII ) UNIV ILLINOIS FOUND.
                                                                                                                                                                                                                            WPI; 2002-500201/53.
                                                                                                                                                                                                                                           N-PSDB; AAD39706
                                                         WO200240501-A2
                Homo sapiens.
Synthetic.
                                                                                     23-MAY-2002.
                                                                                                                                                                                                   Sligar SG,
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AC ADJ70
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                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predasposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

ANURSIO ANURSIO Appresent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; membrane scaffold protein; MSP; phospholipid; nanoscale particle; hydrogel; gold blosensor surface; reproducible assay; crystallisation; biotechnology; pharmaceutical industry; structure determination; bioseparation; drug discovery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 DEPPOSPWDRVKDLATVYVDVLKDSGK----------DSVTSTFSKL 61
                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REQLGPVTQEFWDNLEXETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEBMELYRQK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MSP1D4-5 (helices 4 and 5 deleted) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 476.5; DB 4
Pred. No. 5.9e-32;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 270; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE24648 standard; protein; 168
                                                                                                                                                                                                                                            Drmanac RT;
                                                                                                                                                                      18-APR-2000; 2000US-00552929
26-JAN-2001; 2001US-00770160
                                                                                                                                           16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%;
ilarity 79.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                     WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 94; Conserv
                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 120 AA;
                                                                                     WO200179449-A2
                                                                                                                                                                                   26-JAN-2001;
                                                          Homo sapiens
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                                                                                                               25-OCT-2001
                                                                                                                                                                                                                                         Tang YT,
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Matches
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The invention relates to a membrane scaffold protein (MSP), that self assembles in the absence of phospholipid, with a phospholipid or a mixture of phospholipids, into a nanoscale particle of 5-50 nm in diameter, in an aqueous environment, where the membrane scaffold protein diameter, in an aqueous environment, where the membrane scaffold protein c samphipathic and forms at least one alpha helix. The nanoscale particle comprising MSP is useful for identifying a competitor of binding of a comprising MSP is useful for identifying a competitor of binding of a comprising MSP is useful for identifying a competitor of binding of a competitor protein with MSP, by contacting nanoscale particle and a cereptor protein with a detectable ligand to produce nanoscale particle. Sound detectable ligand contacting the bound ligand with a test compound, and measuring detectable ligand released from the particle, such that a competitor of ligand binding is identified when contacting the bound ligand results in release of the detectable ligand. The cinvention is useful for the incorporation of additional hydrophobic or partially hydrophobic protein molecules. The nanoscale particle can form cage for purification and physical manipulation of disks such as in charties and MSP are useful in biotechnology, pharmaceutical industries and in research areas. The nanoscale particle is useful for structure determination, bioseparation and drug current sequence is MSP1D4-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 MSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 MSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPYSDELRQRLAARLEALKENGGARL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GHHHHHHIBG-----RLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 442.5; DB 5;
Pred. No. 6e-29;
9; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEYHAKATEHLSTLSEKAKPALEDL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 EEMRDRARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ70395 standard; protein; 158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 63.44
Matches 92, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ70395;
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23-OCT-2003

Ghosh SS, Warnock DE;

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New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo Ai in vascular fluid samples and increase LCAT-mediated cholesterol esterification in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The peptides represented in AAR20164-65 are capable of immunologically mimicking an Apo AI epitope. They are useful in diagnosis and detection of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is useful in therapeutic methods for increasing LCAT- mediated cholesterol esterification in humans. The Apo AI polypeptide is selected from the peptides indicated in the features and includes amino acids 13-28 defining a conserved native epitope on Apo AI capable of immunoreacting with monoclonal antibody MAB AI-11. (Updated on 25-MAR-2003 to correct P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 218; DB 2; Length 42; Pred. No. 5.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 QEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAE
                                                                                                                                                         Monoclonal antibody; MAB AI-11; epitope; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.6%; Scott 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 68; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonnet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP76131 standard; protein; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-00534761,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-00534761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCRI ) SCRIPPS CLINIC & RES.
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Conservative
                                                                                                                                                                                                                                                                                                                10. .28
11. .42
11. .28
13. .28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banka CL,
                                                           (revised)
                                                                                                                Apo AI polypeptide (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-007201/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curtiss LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2003
                                                           25-MAR-2003
                                                                             01-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9118619-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1991.
                                                                                                                                                                                                 Synthetic.
                      AAR20164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP76131;
                                                                                                                                                                                                                                                                                             Peptide
Peptide
Peptide
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, encephalopathy lactic acidosis and stroke (MELAS), mycolonic epilepsy ragged red fibre syndrome (MERR) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 MSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
                                                                                           Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel mitochondrial targets that can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                      Human heat mitochondrial protein as a therapeutic target SeqID2201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 437; DB 7; Length 158
                                                                           mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Preu. .v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2201; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 EEMRDRARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                        04-APR-2003; 2003WO-US010870
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BUCK-) BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-845369/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fahy ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 158 AA;
                                                                                                                                                                                                                                                                         WO2003087768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MITO-) MITOKOR
                                                                                                                                                                                                                                      Homo sapiens
06-MAY-2004
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RS;

Smith

2

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Gaps

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Indels

42

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Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;

Human GENSET protein SEQ ID 457.

AAR20164 standard; peptide; 42 AA.

61

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RESULT 12 AAR20164 ID AAR2

Query Match Best Loc Matches

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The peptides represented in AAR20164-65 are capable of immunologically mimicking an Apo AI epitope. They are useful in diagnosis and detection of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is useful in therapeutic methods for increasing LCAT- mediated cholesterol esterification in humans. The Apo AI polypeptide is selected from the features and includes amino acids 6-21 defining a conserved native epitope on Apo AI capable of immunoreacting with monoclonal antibody MAB AI-4. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo Ai in vascular fluid samples and increase LCAT-mediated cholesterol esterification in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; neuroprotective; antiatherosclerotic; antidiabetic; cytostatic; hypotensive; antistyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human apolipoprotein-like ORF717 protein, SEQ ID NO:1434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 163; DB 2;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 KAKVOPYLDDFOKKWOEEMELYROKVEPLRAE 125
                                                                                                                                                                                                Smith RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAKVQPYLDDXQKKWQEEMELYRQKVEPLRAE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                Bonnet DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 68; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP31744 standard; protein; 64
                                                                 90US-00534761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001WO-US017076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2000; 2000US-0206690P
                                                                                                                                                     (SCRI ) SCRIPPS CLINIC & RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Conservative
                                                                                                                                                                                                Curtiss LK, Banka CL,
                                                                                                                                                                                                                                            WPI; 1992-007201/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200190366-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                               07-JUN-1990;
                                                                                                            07-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-2002
                        12-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP31744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1:
ABP31744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ3691) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and bolypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                        New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                      Giordano J;
    toxicity; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
gastrointestinal; gene therapy; GENSET; heavy metal toxicity; or
inflammatory disease; immune disorder; neuromuscular; toxicity;
central nervous system; cardiovascular; gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 65;
                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J, Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; MAB AI-14; epitope; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 22.3%; Score 197; DB 6; I Local Similarity 100.0%; Pred. No. 5.2e-09; es 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 535; 735pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= GLU, PHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR20165 standard; protein; 32
                                                                                                                                                                                                                   18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                18-APR-2001; 2001WO-IB000914,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo AI polypeptide (B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                      Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-075548/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65 AA;
                                                                                                                               WO200283898-A1.
                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                        Homo sapiens
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01-APR-1992
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Best Loca Matches

RESULT 14

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AAR20165

Peptide Peptide Peptide

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Indels

Length 32;

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(CURA-) CURAGEN CORP.
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Leach MD, Shimkets RA;

WPI; 2002-106200/14.

N-PSDB; ABN75770

Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 10; Page 625; 2508pp; English.

Sequences harstvoer-passes, represent 4534, and sequences ABN75054ABN79587 represent cDNAs encoding them. The invention also encompasses
CO Polypeptides at least 80% identical to the ORFY-ORF4534 (collectively
referred to as ORFX) proteins, polymucleotides at least 85% identical to
the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CO Polymucleotides, the recombinant production of ORFX proteins, antibodies
competific for ORFX proteins, methods of detecting ORFX polymucleotides and
polypeptides, methods of screening for modulators of ORFX expression or
competitive, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
competitive and disorder. The ORFX proteins of the invention are used
coll differentiation, immune modulation, haematopoiesis regulation,
clissue growth, anglogenesis, activin, haematopoiesis regulation,
clissue growth, anglogenesis, activin, thrombolytic activity,
combinetic activity, and may also be involved in the determination
of bodily characteristics, fertility and behaviour. ORFX proteins,
cother proliferative disorders may be used in the treatment of cancers,
cother proliferative disorders such as epilepsy and Alzheimer's disease,
corrections of disorders such as epilepsy and Alzheimer's disease,
corrections. organ transplantation, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, storage diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. OFFX nucleic acids may also be used as source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases Sequences ABP31028-ABP35561 represent 4534 novel human proteins 

Sequence 64 AA;

Gaps ; 0 18.3%; Score 162; DB 5; Length 64; 75.0%; Pred. No. 4.2e-06; Live 4; Mismatches 6; Indels Query Match
Best Local Similarity 75.03
Matches 30; Conservative

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41 2 EPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ

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Search completed: December 21, 2004, 10:46:20 Job time : 69 secs

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December 21, 2004, 13:22:55; Search time 144 Seconds (without alignments) 422.444 Million cell updates/sec
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1 DEPPQSPWDRVKDLATVYVD......RARAHVDALRTHLAPYSDEL 170
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1. (cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pept.*)

2. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pept.*)

3. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pept.*)

3. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pept.*)

3. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pept.*)

3. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pept.*)

3. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pept.*)

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4. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pept.*)

5. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pept.*)

6. (cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pept.*)

7. (cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pept.*)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1589859 segs, 357834939 residues
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Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 170
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli	Sequence 729, App	Sequence 29, Appl	Sequence 82, Appl	Sequence 403, App	Sequence 405, App	Sequence 23, Appl	Sequence 2201, Ap	Sequence 81, Appl	Sequence 276814,	Sequence 89, Appl	Sequence 1434, Ap
SUMMARIES	US-09-803-918A-3	US-10-221-278-729	US-10-465-789A-29	US-10-465-789A-82	US-10-038-854-403	US-10-038-854-405	US-10-465-789A-23	US-10-408-765A-2201	US-10-465-789A-81	US-10-424-599-276814	US-10-465-789A-89	US-09-864-408A-1434
	9 4	15	15	15	15	15	15	16	15	15	15	11
* Query Match Length DB	170	166	168	168	93	93	168	158	168	98	43	64
% Query Match	100.0	73.2	59.8	59.8	51.0	51.0	50.0	49.4	44.8	35.9	25.6	18.3
Score	885	647.5	529.5	529.5	451.5	451.5	442.5	437	396.5	318	227	162
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Gaps

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100.0%; Score 885; DB 9; 100.0%; Pred. No. 1.9e-64; tive 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 170; Conservative

Length 170; Indels

1 DEPPGSPWDRVKOLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 1 DEPPQSPWDRVXDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL

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Sequence 21, Appl Sequence 52, Appl Sequence 54, Appl Sequence 54, Appl Sequence 51, Appl Sequence 21, Appl Sequence 10, Appl Sequence 10, Appl Sequence 41, Appl Sequence 33, Appl Sequence 11, Appl Sequence 1129, Appl Sequence 1129, Appl Sequence 1129, Appl Sequence 1129, Appl Sequence 1129, Appl Sequence 1129, Appl	10,48,40,000,000	LING
US-10-120-508-21 US-10-465-799A-52 US-10-465-799A-50 US-10-465-799A-99 US-10-465-799A-99 US-10-465-799A-99 US-10-465-799A-91 US-10-145-239A-10 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11 US-10-142-239A-11	US-10-700-340-37 US-10-142-238A-39 US-10-142-238A-39 US-10-769-787-51 US-10-601-100-44 US-10-142-238A-32 US-10-142-238A-11 US-10-142-238A-11 US-10-142-238A-14 US-10-142-238A-14 US-10-142-238A-14 US-10-142-238A-45 US-10-142-238A-45 US-10-142-238A-45 US-10-142-238A-12 US-10-142-238A-12	SULT 1  Sequence 3, Application US/09803918A  APPLICANT: Bayer, Jenielle  APPLICANT: Bayer, Danielle  APPLICANT: Kohno, Tadahiko  APPLICANT: Kohno, Tadahiko  APPLICANT: Edwarda III, Carl K.  TILE OF INVENTY APPLICATION NUMBER: US/09/803,918A  CURRENT FILING DATE: 2001-07-19  PRIOR FILING DATE: 2001-07-19  PRIOR PLING DATE: 2000-03-13  PRIOR FILING DATE: 2000-03-31  COFTANE: Patentin Ver. 2.1  LENGTH: 170  TYPE: PRT  ORGANISM: Homo sapiens  FEATURE:  LOCATION: (1)- (170)  OTHER INFORMATION: 18 kDa N-terminal fragment  09-803-918A-3
422222222222222222222222222222222222222	7 4 4 0 5 4 4 7 4 4 4 4 4 4 4 6 5 4 4 7 4 4 4 4 4 4 4 4 4 4 4 4 6 4 6 4 6	/09803 chel lie ko Carl K Carl K 5-0000 5-000 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-1 1-07-
252 222 222 222 222 222 222 222 222 222	16 173 173 173 173 188 188 188 198 198 198 198 198 198	A-3 Application US/098 US20020064820A1 US20020064820A1 Dayer, Jan-michel Burger, Danielle Kohno, Tadahiko Edwarda II, Carl RENCE: 06843.0035-00 ELIARIDON NUMBER: ULIAN DATE: 2001-03-13 UCATION NUMBER: 60/NG DATE: 2000-03-13 UGATION NUMBER: 60/NG DATE: 2000-03-13 ON DATE: 2001-03-13 ON DATE: 2000-03-13 ON
2848740966444444		(170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170) (170)
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1132 100 1112 100 1113 96.58 944 96.59	88 89 89 89 89 89 89 89 89 89 89 89 89	RESULT 1 US-09-803-918A-3 US-09-804-803-918A-3 Patent No. US20020064820A1 GENERAL INFORMATION: APPLICANT: Dayer, Jean-Michel APPLICANT: Burger, Danielle APPLICANT: Kohno, Tadahiko APPLICANT: Kohno, Tadahiko TITLE OF INVENTION: APO-A.1 REGULAT FILE REFERENCE: 06843.0035-0000 CURRENT FILLNG DATE: 2001-07-19 PRIOR PILING DATE: 2000-03-13
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Query Match
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                                                                                                                                                                                                               US-10-291-116-7.59, Application US/10291172

Publication No. US20030228584A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REPERENCE: 21272-045

CURRENT APPLICATION NUMBER: US/10/291,172

CURRENT APPLICATION NUMBER: US/10/291,172

CURRENT APPLICATION NUMBER: US/693,267

PRIOR RILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/655,363

PRIOR PRILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/516,847

PRIOR FILING DATE: 2000-06-17

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-06-17

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-03-07

SEQ ID NO 729

LENGTH: 166
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| Publication No. US20040034208A1
| Publication No. US20040034208A1
| GENERAL INPORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
| TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
| TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
| TITLE OF INVENTION: NO. US200400665
| FILE OF INVENTION NUMBER: US/10/221,278
| CURRENT FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
| PRIOR PLING DATE: 2000-09-19
| PRIOR APPLICATION NUMBER: 09/665,363
| PRIOR FILING DATE: 2000-07-14
| PRIOR APPLICATION NUMBER: 09/566,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 130
61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 DEPPOSPWDRVKDLATVYVDVLKDSGK-------DSVTSTFSKL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
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                                                                                121 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 647.5; DB 14
Pred. No. 4.4e-45;
1; Mismatches 3
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Best Local Similarity 82.7%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-729
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61 REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 120
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sligar, Stephen G
APPLICANT: Sligar, Stephen G
APPLICANT: Schuler, Mark
APPLICANT: Schuler, Mark
APPLICANT: Clvian, Natanya R
APPLICANT: Clvian, Natanya R
APPLICANT: Velena V Grinkova
APPLICANT: Velena V Grinkova
APPLICANT: Niia G Denisov
TITULE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
CURRENT APPLICATION NUMBER: 08/10/465,789A
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                          Score 647.5; DB 1
Pred. No. 4.4e-45;
                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        146 EEMRDRARAHVDALRTHLAPYSDEL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: His-tagged MSP1D6
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION UNMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 29, Application US/10465789A; Publication No. US20040053384A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     73.2%;
82.7%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 168
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                                                                                                                                                                                                                                                                                                                                                       Matches 129; Conservative
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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74 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQK 133
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               APPLICANT: Gmither, Ellianda
APPLICANT: Gmither, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFRENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2000-01-22
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PILING DATE: 2001-01-02
PRIOR PELING DATE: 2001-01-02
PRIOR PILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-25
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Pred. No. 2.1e-29;
0; Mismatches 0; Indels 27; Gaps
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Wolenc, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Urial M
APPLICANT: Shimkets, Nichard A
APPLICANT: Shaderna, Steven K
APPLICANT: Gorman, Linda
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Best Local Similarity 77.5%;
Matches 93; Conservative
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Gusev, Vladimir Y
Gangolli, Esha A
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US-10-038-854-403
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.8%; Score 529.5; DB 15; Length 168; Best Local Similarity 74.5%; Pred. No. 1.9e-35; Matches 108; Conservative 5; Mismatches 25; Indels 7;
                  Publication No. US20040053384A1

Publication No. US20040053384A1

GENERAL INFORMATION

APPLICANT: Sligar, Stephen G

APPLICANT: Schuler, Mary A

APPLICANT: Schuler, Mary A

APPLICANT: Schuler, Mary A

APPLICANT: Yelena V. Grinkova

APPLICANT: ON WINBER: US/10/465,789A

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: 60/252,233

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/252,233

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.1

SEQ ID NO 82

LENGTH: 168
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115 AEYHAKATEHLSTLSEKAKPALEDL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: His-tagged MSP1D6D7
US-10-465-789A-82
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Publication No. US20040022781A1
GENERAL INFORMATION:
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Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Bisen, Andrew J
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Rastelli, Luca
Casman, Stacie J
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Gusev, Vladimir Y
Gangolli, Esha A
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US-10-465-789A-82
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TYPE: PRT
CORGANISM: Homo sapiens
US-10-408-765A-2201
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                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DSVTSTFSKLREQLGPVTQEFWD 33
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                                                                                                                                                                                                                      14 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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                                                                                                                                                            APPLICANT: MacDougall, John R IIILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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US-10-465-789A-23
i Sequence 23. Application US/10465789A
j Publication No. US20040053384A1
gENERAL INFORMATION:
i APPLICANT: Sligar, Stephen G
j APPLICANT: Schuler, Mary A
j APPLICANT: Schuler, Mary A
j APPLICANT: Yelena V. Grinkova
j APPLICANT: Ilia G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
j FILE REFERENCE: 87.00A
j CURRENT APPLICATION UNBER: US/10/465,789A
j CURRENT FILING DATE: 2003-06-18
                                                                                                                                                                                     FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
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                                                        Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
                                                                                                                              Smithson, Glennda
Millet, Isabelle
                                            Casman, Stacie J
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APPLICANT:
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96 MSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKDLBEVKAKVOPYLDDFOKKWOBEMELYROKVBPLRABLOBGAROKLHELOEKLSPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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Bublication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Zhang, Bing
APPLICANT: Glenn, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Haylor, Steven W.
APPLICANT: Haylor, Steven W.
APPLICANT: Glenn, Gary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDEMTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 1DEMTIFIED IN THE MITOCHONDRIAL PROTEOME
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49.4%; Score 437; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.2e-28;
Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 442.5; DB 15; Length
Pred. No. 2.4e-28;
9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2201
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 EEMRDRARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 AEYHAKATEHLSTLSEKAKPALEDL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 EEMRDRARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: His-tagged MSP1D5D6
US-10-465-789A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEMRDRARAHVDALRTHLAPYSDEL 85
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-10-465-789A-81
Sequence 81, Application US/10465789A
; Publication No. US20040053384A1
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.4%;
Matches 92; Conservative 5
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 1434, Application US/09864408A

Sequence 1434, Application US/09864408A

Sequence 1434, Application US/09864408A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Bhimkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides EncryRein APPLICATION NUMBER: US/09/864,408A

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 60/206,690

PRIOR APPLICATION NUMBER: 60/206,690

NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.6%; Score 227; DB 15; Best Local Similarity 100.0%; Pred. No. 1.8e-11; Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                              APPLICANT: Sligar, Stephen G
APPLICANT: Sligar, Stephen G
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Cloyan, Natanya R
APPLICANT: Velena V. Grinkova
APPLICANT: Ilia G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
TITLE OF INVENTION: Membrane Scaffold Proteins
TITLE OF INVENTION: Membrane Scaffold Proteins
CURRENT FILING PIET: 2003-06-18
CURRENT FILING DATE: 2003-06-18
FRIOR FILING DATE: 2001-11-20
FRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                   ; Sequence 89, Application US/10465789A; Publication No. US20040053384A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: sequence of GLOB
US-10-465-789A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 30; Conservative
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ORGANISM: Homo sapiens
  RE 62
                                                    85 ŘE 86
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US-09-864-408A-1434
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                                                                                                                                     RESULT 12
US-10-465-789A-89
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LENGTH: 43
61
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SPERIOR E: 38-21 (53.23.3) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ERNGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------PLGEEMRDRARAHVDALRTHL 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
44.8%; Score 396.5; DB 15; Length 168;
Best Local Similarity 65.4%; Pred. No. 1.4e-24;
Matches 83; Conservative 0; Mismatches 0; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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US-10-424-599-276814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: artificial sequence of MSP1D4D5
US-10-465-789A-81
           APPLICANT: Sligar, Stephen G
APPLICANT: Sligar, Stephen G
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Maranya R
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Tila G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
CURRENT APPLICATION NUMBER: 08/990,087
PRIOR FILING DATE: 2003-06-18
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 81
LENGHR: 168
TYPE: PRT
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Sequence 21, Application US/10120508

Sequence 21, Application US/10120508

Publication No. US20030191057A1

GENERAL INFORMATION:

APPLICANT: FORGELMAN

TITLE OF INVENTION: G-TYPE PEPTIDES TO AMELIORATE ATHEROSCLEROSIS

FILE REFERENCE: 407T-301100US

CURRENT APPLICATION UNMBER: US/10/120,508

CURRENT PILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.0

SEQ ID NO 21

LENGTH: 26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.8%; Score 122; DB 15; Length 22; Best Local Similarity 100.0%; Pred. No. 0.0029; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GESTOR 15.789A-52

Sequence 52, Application US/10465789A

Publication No. US20040053384A1

GENERAL INPORMATION:
APPLICANT: Sligar, Stephen G

APPLICANT: Schuler, Mary A

APPLICANT: Schuler, Mary R

APPLICANT: Yelena V. Grinkova

TITLE OF INVENTION: Membrane Scaffold Proteins

FILE REFERENCE: 87-00A

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: 09/990,087

PRIOR APPLICATION NUMBER: 60/252,233

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: 22
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; OTHER INFORMATION: Synthetic D peptide.
US-10-120-508-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 WDRVKDLATVYVDVLKDSGRDYVSQF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 PYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Search completed: December 21, 2004, 13:39:57 Job time : 145 secs

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RESULT 1
US-08-292-870-1
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Sequence 2, Appli
Sequence 4, Appli
Sequence 105, App
Sequence 92, Appl
Sequence 92, Appl
Sequence 520, App
Sequence 520, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 129, Appli
Sequence 149, Appli
Sequence 18, Appli
Sequence 2, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 13, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 13, Appli
                                                                         December 21, 2004, 13:37:37 ; Search time 39 Seconds (without alignments) 289.078 Million cell updates/sec
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                                                                                                                              US-09-803-918A-2_COPY_25_194
885
1 DEPPQSPWDRVKDLATVYVD......RARAHVDALRTHLAPYSDEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Re_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-248-796A-16325
US-08-182-175A-87
PCT-US92-06412-87
US-08-365-103B-14
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US-08-292-870-3

US-08-292-870-4

US-08-292-870-4

US-08-182-175A-105

US-08-474-33A-92

US-08-433-771-92

PCT-US92-06412-105

US-07-649-389-7

US-07-959-946-5

US-07-959-946-5

US-07-959-946-5

US-07-959-946-5

US-07-959-946-5

US-07-959-946-5

US-09-333-577-5

PCT-US92-08634-5

US-09-079-030-129

US-09-079-030-129

US-09-079-030-129

US-09-133-999C-5882

US-09-133-999C-5882

US-09-133-999C-5882

US-09-133-990C-5882

US-09-133-999C-5882

US-09-133-990C-5882

US-09-133-990C-5882

US-09-133-990C-5882

US-09-133-990C-5882

US-09-137-97-77-3734

US-09-270-767-3733
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                             478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                    OM protein
                                                                                                                                                             Sequence:
                                                                                                                                                                                                                             Searched:
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                                                                             Run on
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28 77.5 8.8 167 1 US-08-365-103B-12 Sequence 12, Appl 29 77.5 8.8 144 4 US-09-270-767-62028 Sequence 62028, A 30 77.5 8.8 164 4 US-09-270-767-59203 Sequence 62028, A 31 76.5 8.6 114 4 US-09-219-990-6218 Sequence 6218, Appl 34 76 8.6 114 4 US-09-513-9990-524 Sequence 5524, Appl 34 76 8.6 114 4 US-09-513-9990-6218 Sequence 18411, A 36quence 6681, Appl 36 74.5 8.4 105 4 US-09-513-9990-681 Sequence 6681, Appl 36 74.5 8.4 157 4 US-09-210-9900-681 Sequence 6681, Appl 37 73.5 8.3 99 4 US-09-270-767-41567 Sequence 6681, Appl 40 US-09-270-767-41567 Sequence 50148, Appl 41 73 8.2 144 4 US-09-270-767-34931 Sequence 50148, Appl 41 73 8.2 144 4 US-09-270-767-50148 Sequence 50148, Appl 41 73 8.2 165 4 US-09-270-767-50148 Sequence 571, Appl 42 73 8.2 165 4 US-09-270-767-50148 Sequence 571, Appl 44 72 165 4 US-09-898-54-24 Sequence 24, Appl 44 72 8.1 108 2 US-08-710-767-59533 Sequence 24, Appl 71.5 8.1 108 2 US-08-710-767-59533 Sequence 24, Appl 545 71.5 8.1 108 2 US-08-710-749-24 Sequence 24, Appl
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# ALIGNMENTS

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US-09-39-80-1

Sequence 1, Application US/08292870

APPLICANT: Smith, Actard Solids L

APPLICANT: Smith, Actard Solids Research Institute, Office of ADDRESSES: The Scripps Research Institute, Office of COMPRESSES: The Scripps Research Institute, Office of Solids L

SONFRESSED READABLE FORM:

COUNTRY: La Jolia

STATE: California

CONFUTER: INP PC Compatible

CONFUTER: INP PC COMPATIBLE FORM:

MARIER PRINCATION NUMBER: US 07/534,761

PRINCA APPLICATION NUMBER: US 07/534,761

PRINCA APPLICATION NUMBER: TSTUS 91/04038

FILING DATE: 07-01W-1991

ATTORNEY/BERNEY/BERNEY PRINCATION NUMBER: TSTUS 91/04038

FILING DATE: 07-01W-1991

ATTORNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNEY/BERNE
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OPOLOGY:
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                                                                                                                                                                                                                            US-08-292-870-3
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                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
ITILE OF INVENTION: APO AL POLYPEPTIDES, DIAGNOSTIC METHODS
ITILE OF INVENTION: METHODS
ITILE OF INVENTION: METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
                                                                                                                                                                                                      85 EMSKDLEEVKAKVQPYLDDFQKKWQEEMBLYRQKVEPLRAELQEGARQKLHELQEKLSPL 144
                                                                                                                                                                                                                              1 EMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPL 60
                                                                                                                                                            0; Gaps
                                                                                                               Length 64;
                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSITCATION: 436
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/711,333
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY AGENT INFORMATION:

NAME: Fitting, Thomas
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ 1D NO: 2:

SEQUIRCE CHARACTERISTICS:
                                                                                                          Query Match 37.1%; Score 328; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 64; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08292870 Patent No. 5814467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-2
                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                              145 GEEM 148
                                                                                                                                                                                                                                                                                                                                  GEEM 64
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                                                               US-08-292-870-1
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Patent No. 5814467

GENERAL INFORMATION:

APPLICANT: Curitiss, Linda K

APPLICANT: Banka, Carole L

APPLICANT: Smith, Richard S

TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS

TITLE OF INVENTION: METHODS

TITLE OF INVENTION: METHODS

TITLE OF INVENTION: METHODS

TITLE OF SEQUENCES: 4

NUMBER OF SEQUENCES: 4
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Query Match 25.6%; Score 227; DB 2; Length 44; Best Local Similarity 100.0%; Pred. No. 1e-13; Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
18.4%; Score 163; DB 2; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.9e-08;
Matches 31; Conservative 0; Mismatches 1; Indels
                                                                                                                        83 ROEMSKDLEEVKAKVOPYLDDFOKKWOEEMELYROKVEPLRAEL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STRET: 1066 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
                                                                                                                                                               1 RQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 11

OTHER INFORMATION: /note= "Xaa can be either E (Glu);
OTHER INFORMATION: or F (Phe)"
15. OTHER INFORMATION: Or F (Phe)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION NUMBER: US 07/534,761
FILING DATE: 07-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: FILLING THOMAS
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 150.1 D1
TELECOMMUTICATION INFORMATION:
TELEFACOMMUTICATION INFORMATION:
TELEFACOMMUTICATION NUMBER: TSRI 210.1 D1
TELEFACOMMUTICATION NUMBER: 150-554-297
TELEFACOMMUTICATION SEQ 1D NO: 3:
CFOTTENTER CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
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SENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                         ADDRESSEE:
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                                                                                                                                             Sequence 4, Application US/08292870

Batent No. 5814467

CENERAL INFORMATION:
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
ITILE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
ITILE OF INVENTION: METHODS
ITILE OF INVENTION: METHODS
ITILE OF INVENTION: METHODS
AUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTREN: IBM PC compatible
CORPTREN: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
FILING DATE: 07-AUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-AUN-1991
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-AUN-1991
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-AUN-1991
ATFORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEFPKN: 619-554-2937
THEREPARK: 619-554-2937
THEREPARK: FOR 510 NO. 4.
94 KAKVQPYLDDFQKKWQEEMELYRQKVEPLRAE 125
                                1 KAKVQPYLDDXQKKWQEEMELYRQKVEPLRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 SKDLEEVKAKVQPYLDDFQKKWQEE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 96.0
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
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US-08-182-175A-105
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APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTON: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 EMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 106.5; DB 1; 27.3%; Pred. No. 0.02; tive 28; Mismatches 35;
                                                                                                                                      B: E.I. du Pont de Nemours and Company
1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: NETHODS FOR INCREASING
TITLE OF INVENTION: NOTHERONINE CONTENT
TITLE OF INVENTION: AND THREONINE CONTENT
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: R. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System,
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-474-633A-92
; Sequence 92, Application US/08474633A
; Patent No. 5773691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 835420
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4229
TELEPAK: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.3*
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-182-175A-105
                                                                                                                                                           STREET: 1007 Marke
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILMINGTON
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 EMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 KWKVMEEKWKKLE-EKMKAMEDKWKWLEEKWKKLEEKMK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.0%; Score 106.5; DB 1;
Best Local Similarity 27.3%; Pred. No. 0.02;
Matches 27; Conservative 28; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: WILMINGTON
CITY: WILMINGTON
STATE: DELAWRE
COUNTRY: U.S.A.
ZIP: 1999
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Max-1997
CLASSIFICATION: cUnknown>
PRIOR APPLICATION MARSER: 08/474,633
PILING DATE: ALMKNOWN>
PRIUM TAPPLICATION NUMBER: 08/474,633
PILING DATE: AUKNOWN>
PILING DATE: AUKNOWN>
PILING DATE: AUKNOWN>
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INCREASING THE LYSINE
AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . DU PONT DE NEMOURS
                        ZIF: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:
RICHARDY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
RECISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: B. I. DU PONT DE NEMOURS AND COMPANY TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1007 MARKET STREET
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; Sequence 92, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 302-773-0164
TELEX: 835-420
INFORMATION FOR SEQ ID NO: 92: SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: 1 inear
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ADDRESSEE: B. I. D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-474-633A-92
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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Sequence 105, Application PC/TUS9206412

GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 KLKEEMAKOKDEMWKLKEEMKKLEEKWKVMEEKMKKLEEKKMKAMEDKOKWKLEE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 EMELYROKVEPLRAELQEGAROKLHELQEKLSPLGEEMR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSER: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30,684

RECERENCE/DOCKET NUMBER: BB-1037-C

TELEPHONE: 302-992-4931

TELEPHONE: 302-992-4931

TELEPHONE: 302-992-4931

TELEPHONE: 835420

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TYPE: protein

SEQUENCE TYPE: protein

SEQUENCE TYPE: protein

SEQUENCE TYPE: DESCRIPTION: SEQ ID NO: 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: UDSA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY AGENT INFORMATION:
TELECOMMUNICATION NUMBER: BB-1031
TELEFAN: (302) 992-4929
TELEFAX: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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COUNTRY: USA
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58 SKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Dan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 ŚELEBÓLTPVAEBTRARLSKELQAABAPLGADMBDVRGRLVQY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 100; DB 1; Length 110; 26.6%; Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 180 No. 5408038th Stetson, Suite 4700 CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16787/168/DFBC
TELECOMMULTOATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)693-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: 133
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-UNU-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERNICE/DOCKET NUMBER:
TELEPHONE: (312)616-5400
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07959946
Patent No. 5408038
                                                                                                                                                                                       TELBEAK: (700,
TELEFAX: 870149
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
""DE: AMINO ACID
""DE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Conservative
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                                         19920519
                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-07-849-389-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler,
ADDRESSEE: Milnamow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                         APPLICATION NUMBER:
FILING DATE: 199205
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                       59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                ,
6
  DB 5; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Indels
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 RQLQEELEEVKARLQPYM-----AEAHELVGWNLEGLR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 QEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLR 123
                                                                                                                                                                            111 EMELYROKVEPLRAELOEGAROKLHELOEKLSPLGEEMR 149
                                                                                                                                                                                                                   67 KMKVMEEKMKKLE-EKMKAMEDKMKWLEEKMKKLEEKMK 104
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO S. 2220
LENGTH: 128
                                         35;
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Patent No. 5526493
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
STATE: Virginia
                      .02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.4%; Score 101; DB 4
Best Local Similarity 29.0%; Pred. No. 0.08;
Matches 29; Conservative 22; Mismatches
                         27.3%; Pred. No. 0.02
:ive 28; Mismatches
  12.0%; Score 106.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                            Sequence 5220, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i LOCATION: 104
; OTHER INFORMATION: Xaa = His,Gln
US-09-621-976-5220
                    Best Local Similarity 27.3
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: -23..-1
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                          US-09-621-976-5220
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  Query Match
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                                                                                                                                셤
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Smith, Richard K.

APPLICANT: South, Raju

APPLICANT: Young, Stephen G.

APPLICANT: Witztum, Joseph L.

APPLICANT: Witztum, Joseph L.

APPLICANT: Witztum, Linda K.

TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                10.3%; Score 91; DB 1; Length 16; 100.0%; Pred. No. 0.047; tive 0; Mismatches 0; Indels
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ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,577
FILING DATE:
CLASSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700 CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08333577
Patent No. 5786206
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Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
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; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHRACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: AMINO ACID

; MOLECULE TYPE: protein

US-07-959-946-5
                                                                                                                                                                                                                                                                                                            Query Match 10.3%
Best Local Similarity 100.0°
Matches 16; Conservative
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MOLECULE TYPE: protein
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RESULT 13 PCT-US92-08634-5

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Sequence 5, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Young, Stephen G.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Dan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
CONTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UNMER: PCT/US92/08634
FILING DATE: 19921009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 91; DB 5; Lei
100.0%; Pred. No. 0.047;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03/901,706
FILING DATE: 18-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TELEFAX: (312) 616-5400
; TELEFAX: (312) 616-5400
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino Tryen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 KVQPYLDDFQKKWQEE 111
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Matches 16; Conservative
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MOLECULE TYPE: protein
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US92-08634-5
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Search completed: December 21, 2004, 13:52:13
Job time : 40 secs
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APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REPERENCE: PATHOU-OTA

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1998-06-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3496

LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 EQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Indels 26; Gaps
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10.1%; Score 89; DB 4; Length 114;
Best Local Similarity 25.0%; Pred. No. 0.82;
Matches 26; Conservative 24; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::|:| | | : | | : ::||:| 52 SAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARM 95
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: CONCURTENTLY Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCM111an, Nabeela R.
FEGISTRATION NUMBER: P-43.363
REFERENCE/DOCKET NUMBER: ARAG:003
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/414-757
SEQUENCE CHARACTERISTICS:
FRANCTH: 114 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |: : | |: : | |: : : | |: : : | | |: 83 ILAQAKSYAFQATEASKNQLNNLKEQWQEKAEALDDS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT CRGANISM: Streptococcus pneumoniae US-09-583-110-3496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 114 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-129
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US-09-583-110-3496
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December 21, 2004, 13:19:15 ; Search time 38 Seconds (without alignments) 303.842 Million cell updates/sec
                                                                                                                                                                                                                                                 1 DEPPQSPWDRVKDLATVYVD......LDDFQKKWQEEMELYRQKVE 120
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          283416 seqs, 96216763 residues
                                                                                                                                                                                              US-09-803-918A-2_COPY_25_144
631
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                          Run on:
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52135

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 120

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

conserved hypothet hypothetical prote ski-replated protei kinetoplastid memb hypothetical prote finetoplastid memb flagallar protein neurofilament-M ho hypothetical prote hypothetical prote virulence-associat hypothetical prote integral membrane hypothetical protein hypothetical protein hypothetical protein prote prote hypothetical prote antifreeze protein hypothetical prote nonhistone chromos conserved hypothet apolipoprotein AI apolipoprotein A-I prote prote prote apolipoprotein A-I hypothetical prote probable molybdopt hypothetical hypothetical hypothetical hypothetical hypothetical Description SUMMARIES \$67972 A56866 A05313 B69818 G86722 B46598 S53443 C89923 S53442 I140399 A60094 C86901 F71511 H64112 C90261 I68742 B82904 C90342 A59010 H81298 D95153 H97483 D75111 D82445 JU0038 F81669 H71978 四 Query Match Length Score 59.5 59.5 59.5 59.5 Result Š

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Gaps

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8

DPPQTPLDRIRDMLDVYLETVKASGKDAISQFESSA 36 EPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 37

2; Length 36;

16.8%; Score 106; DB 2, 50.0%; Pred. No. 0.032; 10; Mismatches

18; Conservative

7

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Query Match Best Local Similarity Matches 18; Conserva

hypothetical prote conserved hypothet hypothetical prote apolipoprotein A-I hypothetical cytos hypothetical 10.0 transposase BMEIIO transposase BMEIIO transposase BMEIIO hypothetical protein conserved hypothetical prote hypothetical hyp	RESULT 1  SALIGNMENTS  RESULT 1  Sport 1  Sport 2  Sport 3  Sport 4  Sport 4  Sport 4  Sport 4  Sport 5  Sport 5  Sport 5  Sport 5  Sport 5  Sport 5  Sport 6  Sport 6  Sport 6  Sport 7  Sport 6  Sport 7  Sport	re 106; DB 2; Length 34; d. No. 0.03; Mismatches 6; Indels 0; Gaps 0; sGRDYVSQFE 34   :  ::    SGRDYLAQFE 33	RESULT 2 A56866 apolipoprotein A-I - Japanese quail (fragment) C;Species: Coturnix coturnix japonica (Japanese quail) C;Species: Coturnix coturnix japonica (Japanese quail) C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: A56866 R;Oku, H.; Ishikawa, M.; Nagata, J.; Toda, T.; Chinen, I. Biochim. Biophys. Acta 1167, 22-28, 1993 A;Title: Lipoprotein and apoprotein profile of Japanese quail. A;Reference number: A56866; MUID:93213845; PMID:8461329 A;Accession: A56866 A;Accession: A66866 A;Accession: A66866 A;Accession: A66866 A;Accession: A66866
AB1425 AB0012 DG7844 DG7734 AB3643 AB3643 AB3633 AB90187 AD1533 AD1533 AD1533 AD1533 AD1533 AD1533 AD155 AD155 AD155	ALIGRALICS  or of the control of the	Score 106; Pred. No. 9; Mismatc VLKDSGRDYVS :    :  ::  TVKASGRDYL	il (fraginica (Jē ision 16 J.; Jodē 8, 1993 in profij 9321384! 8
0000000000000000	agme Lic Lrev Juss 1997RR	8%; 5%; VYUD VYLE	quail japonic _revisi Ea, J. 22-28, 22-28, 12-28, 10:93, 32918 32918 32918 A prima
120 102 102 103 111 110 100 110	goose (fragmen ser (domestic ghasquence_revi) sequence_revi) set, N.; Rousse to 596-591, 199 sation of apoli; S67972; MUID:9 yr	16.8% 54.5% vative VKDLATVYY :       LKDLVDVYI	Japanese coturnix jisequence—M.; Nagat an 1167, 2 and apoption for the first seed from the form and found was found opprotein optrotein social from the found for the first seed from the found for the first for the first found for the first
a a a a a a a a a a a a a a a a a a a	BESULT 1  6.7992  polipoprotein AI - goose (fragment)  posecies: Anser anser (domestic goose)  pace: 14-Feb-1997 #sequence_revision  pace: 14-Feb-1997 #sequence_revision  pace: 15-Feb-1997  in in in it is seallier, N.; Rousselot-Febranier, D.; School, Sept. 1995  pace and the pace of the pa	h Similarity 54.5%; Pred. No. 0.0  18; Conservative 9; Mismatches  2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE  1	A-I - Ja rinix cot 1995 #se 6866 kawa, M. W. Acta Octein an minary minary e octein wa extract
0. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8.	roctein ss. Anses 14-Peb- tion: Se Biochem Charac Charac tion: Se ii: prelii te type le type amily:	atch cal S 16	urotein se: Cotulion: Asylvinon:
W W W W W W W W W A A A A A A A A A A A	RESULT 1 S67972 apolipoprotein AI - g C; Species: Anser anse C; Date: 14-Feb-1997 # C; Accession: S67972 R; Hermier, D.; Sellie Eur. J. Biochem. 234, A; TReference number: SA; Reference number: SA; Reference number: SA; Reference number: SA; Residues: 1-34 cHER A; Cross-references: UC; Superfamily: apolip	Query Match Best Local Matches 1 Qy 2 Db 1	RESULT 2 A56866 apolipoprotein A-I C;Species: Coturni C;Date: 18-Aug-199 C;Accession: A5686 R;Oku, H.; Ishikaw Biochim. Biophys. A;Title: Lipoprote A;Reference number A;Reference A;Cress: references A;Note: sequence A;Note: sequence A;Note: this prote C;Superfamily: apo

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Ribolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Bhrli Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-79 <STO>
A,Cross-references: UNIPROT:Q9CHE9; GB:AE005176; PID:g12723703; PIDN:AAK04881.1; GSPDB:C
A,Experimental source: strain IL1403
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rijardim, A.; Funk, V.; Caprioli, R.M.; Olafson, R.W.
Biochem. J. 305, 307-313, 1995
A;Title: Isolation and structural characterization of the Leishmania donovani kinetoplas
hypothetical protein yhjA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C.Species: Lactococcus lactis subsp. lactis C.Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C.Accession: G86722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 INLKLIDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 QLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LNDKLDATKOKVS---GKVKETTGKVTGDEKLEAKGKTEGLMGKAKEGLENIKDKASDLA 59
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kinetoplastid membrane protein-11 - Leishmania donovani
C;Species: Leishmania donovani
C;Species: Leishmania donovani
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession: $5344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exi-related protein SnoN - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Species: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B46598
R;Nagase, T.; Nomura, N.; Ishii, S.
J. Blol. Chem. 268, 13710-13716, 1939
A;Fitle: Complex formation between proteins encoded by the ski gene family.
A;Reference number: A46598; MUID:93293901; PMID:8514802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Notes: sequence extracted from NCBI backbone (NCBIP:134568, NCBIP:134572)
C;Superfamily: ski transforming protein
C;Keywords: DNA binding; tandem repeat
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ش
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 76.5; DB 2; Length 7; Pred. No. 15; 16; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LD-----DFQKKWQEEMELYRQKVE 120
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1 Similarity 29.1%;
23; Conservative 1
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Best Local Similarity
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Best Local Similarity
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Cispecies: Bace-1997
Cispecies: Ci
                                                                                                                                     C;Species: Errthrocebus patas (red guenon, hussar)
C;Species: Errthrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
Accession: A05313
B;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
B;Ochemistry 15, 1928-1933, 1976
A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus A;Mccession: A05313
A;Molecule type: protein
A;Mcsession: A05313
A;Molecule type: protein
A;Mcsession: A05313
A;Molecule type: protein
A;Coss-references: UNIPROT:P18647
C;Superfamily: apolipoprotein A-1
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 101; DB 2;
85.0%; Pred. No. 0.04;
iive 2; Mismatches 1
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                                                                      apolipoprotein A-I - red guenon (fragment)
N,Alternate names: apo-A-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| : ||||||| :: ::| ::
LQTSI----KKWQEEIKPHQQDLO 99
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Best Local Similarity 85.00,
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Best Local Similarity
Matches 22; Conserv
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flagellar protein filt - Bacillus subtilis
C'Species Bacillus subtilis
C'Species Bacillus subtilis
C'Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C'Accession: 140399; F69525
R'Chen, L.; Helmann, J. D.
R. Bacteriol. 176, 3093-3101, 1994
A'Fitle: The Bacillus subtilis sigma D-dependent operon encoding the flagellar proteins
A,Reference number: 140396; MUD:94252974; PMID:8195064
A,Fitle: The Bacillus subtilis sigma D-dependent operon encoding the flagellar proteins
A,Reference number: 140396; MUD:94252974; PMID:8195064
A,Reference number: 140396; MUD:94252974; PMID:8195064
A,Reference: UNIRPOT:P39740; EMBL:231376; NID:9499379; PIDN:CAA83250.1; PID:9499
A,Reference: UNIRPOT:P39740; EMBL:231376; NID:9499379; PIDN:CAA83250.1; PID:9499
A,Rust, F.; Ogaswarx, N.; Moszer, I.; Albertini, A. M.; Alloni, G. Ascwedo, V.; Berrick,
C.; Bron, S.; Brutillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N. M.; Ch.
A; Ehrlich, S.D.; Bammerson, P. T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle,
A,Authors: Foulger, D.; Fritz, C.; Rumano, M.; Runta, K.; Japidus, A.; Baucel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudeay, B.; Rose, M.; Sadaie, Y.; Sato, T.; Satonlon,
A,Authors: Jubber, J.; Hanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uchiyama,
A,Authors: Schleich, S.; Schreter, E.; Scoffene, F.; Sekiguchi, J.; Sekowska, A.; Sato,
A,Authors: Yoshikawa, H.P.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A; Raider, P.; Miller, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Miller, P.; Combitawa, A.; Miller, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Miller, B.;
A,Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A,Ruthors: Positikawa, H.P.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A; Readerence number: R69253
A; Genetics:
A; Genetics
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R;Sharpe, C.R.
Revelopment 103, 269-277, 1988
A;Title: Developmental expression of a neurofilament-M and two vimentin-like genes in X A;Reference number: A60094; MUID:89136789; PMID:3224553
A;Accession: A60094
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 4 IDQLYTETKSMLSHIQNTPESDEL-LKQIRDF---VATRSELIQEISLPLSEERRQMKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 113;
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24; Conservative
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Best Local S:
Matches 24
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C;Species: Leishmania donovani
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession. 553442
B;Jardim, A.; Hanson, S.; Ullman, B.; McCubbin, W.D.; Kay, C.M.; Olafson, R.W.
Biochem. J. 305, 315-320, 1995
A;Title: Cloning and structure-function analysis of the Leishmania donovani kinetoplasti
A;Reference number: S53442
A;Accession: S5442
A;Statuus: preliminary
A;Statuus: preliminary
A;Residues: 1-92 cJAR>
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A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ciaccasion: C89923

R. Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A.Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Recession: C89923

A;Accession: C89923

A;Status: preliminary
A;Residues: 1-113 < kurs.
A;Residues: 1-113 < kurs.
A;Residues: 1-113 < kurs.
A;Cross-reference unipror: Q99U38; GB:BA000018; PID:g13701249; PIDN:BAB42544.1: GSPD
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                                                                                                                                                                                                                                                                                                                              51 DSVTSTFS-KLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 109
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                                                                                                                                                                                                                                                                                                                                                                          2 DRLDBEFNRKMQEQ-----NEFADKPDEST--LSPEMREHYEKFERMIKEHTEKFNKKMH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein [imported] - Staphylococcus aureus (strain N315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 2; Length 113
Pred. No. 1.5e+02;
9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|:|:||||:|::|
4 ITKEVFDNLEQEIDVFAKNKALGSSEAK----PYLDEYHSK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinetoplastid membrane protein-11 - Leishmania donovani
A; Reference number: S53443; MUID:95126922; PMID:7826346
                                                                                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 65.5; DB 2; 24.3%; Pred. No. 1.3e+02;
                                                                                                                                                                                            DB 2;
                                                                                                                                                                                        Query Match
10.9%; Score 69; DB 2
Best Local Similarity 29.0%; Pred. No. 59;
Matches 20; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
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Best Local Similarity 34.1%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 EEMELYRQK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHSEHFKÖK 63
                              A;Accession: S53443
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-79 <JAR>
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Matches 18; Conserv
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Virulence-associated protein vapA homolog HI1251 - Haemophilus influenzae (strain Rd KW2 C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Placenmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Grahm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64112
A;Status: nucleic acid sequence not shown; translation not shown
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A;Cross-references: UNIPROT:Q57089; GB:U32805; GB:L42023; NID:g1574180; PIDN:AAC22901.1;
C;Superfamily: virulence-associated protein vapA
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SSO1086 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: C90261 C;Accession: C
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A;Cross-references: UNIPROT:Q97Z50; GB:AE006641; NID:g13814276; PIDN:AAK41346.1; GSPDB:G
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llarity 32.5%; Pred. No. 2.9e+02;
Conservative 15; Mismatches 21; Indels
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10.0%; Score 63; DB 1; 1
Best Local Similarity 23.9%; Pred. No. 2.4e+02;
Matches 22; Conservative 21; Mismatches 31
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nes 25; Conserv
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C.Species: Chlamydia trachomatis
C.Species: Chlamydia trachomatis
C.Species: Chlamydia trachomatis
C.Species: Chare: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C.Accession: F71511
C.Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A,Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach, Reference number: A71570; MUD:99000809; PMID:9784136
A,Refatus: F71511
A,Status: P71511
A,Status: DAA
A,Molecule type: DNA
A,Molecule type: UNPROT:084472; GB:AE001320; GB:AE001273; NID:g3328891; PIDN:AAC6806
A,Experimental source: serotype D, strain UW-3/Cx
A,Generics:
C,Generics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypotherical protein ywjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis C; Manager, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A; Reference number: A86625; MUID:21235186; PMID:11337471
A; A; Ression: C86901
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-115 <STO>
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A;Experimental Bource: strain IL1403
C;Genetics:
A;Gene: ywjB
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                                                                                                                                                                                                                                                                            13 DLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQE-- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 VSQFEGSALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKD 89
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     Length 104;
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Query Match 10.2%; Score 64.5; DB 2; Length 1 Best Local Similarity 24.0%; Pred. No. 1.8e+02; Matches 24; Conservative 18; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           75 LEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMEL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 LDNELRGTKWEMSRHLRE-----YQDLLLNVKWALDIEI 101
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C;Superfamily: conserved hypothetical protein CP0165
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Search completed: December 21, 2004, 13:31:26 Job time : 40 secs

Mis Pose Blonk (USDIO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein December 21, 2004, 13:19:55; Search time 190 Seconds Run on:

(without alignments) 363.395 Million cell updates/sec

US-09-803-918A-2_COPY_25_144 631 1 DEPPQSPWDRVKDLATVYVD......LDDFQKKWQEEMELYRQKVE 120 score: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 120

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	002762 ovis aries	Q61d50 mus sp. apo		Q29248 sus scrofa	Q9uct8 homo sapien		P18647 erythrocebu	Q9qv04 rattus sp.		Q28995 saimiri sci	007516 bacillus su	Q7p280 fusobacteri		Q9pss3 gallus gall		O68958 streptococc		Q6whj6 bacteriopha		Q8Ir54 bacillus an		Q8iif8 plasmodium	Q7yzc6 trypanosoma	Q29258 sus scrofa	Q9gu60 leishmania	Q9zfz1 streptococc	Q26773 trypanosoma	Q7yzc5 trypanosoma	Q9xzh5 leishmania		Q91cr0 paenibacill
ID	002762	Q6LD50	AAB35539	Q29248	Q9UCT8	Q9PRR6	APA1 ERYPA	Q9QV04	APE MACMU	APE SAISC	007516	Q7P280	09СНЕ9	Q9PSS3	068959	068958	Q9PXP4	Фемнле	AAQ64377	Q81R54	AAT31321	QBIIFB	Q7YZC6	029258	Q9GU60	Q9ZFZ1	KM11_TRYBB	Q7YZC5	Q9XZH5	054892	Q9LCR0
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Length	56	79	79	82	56	34	20	30	107	107	118	96	79	66	118	117	102	16	76	93	93	113	92	102	92	114	92	92	92	104	90
* Query Match	39.1	35.8	35.8	34.4	22.3	16.8	16.0	16.0	13.5	13.2	12.8	12.3	12.1	12.0	12.0		11.8	11.6	11.6	11.6	11.6	11.6	11.4	11.4	11.2		11.1		11.0	10.9	10.8
Score	247	226	226	217	141	106	101	101	82	83	81	77.5	76.5	9/	92	75	74.5	73	73	73	73	73	72	72	70.5	70.5	70	70	69.5	69	68
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Q6bmu6 debaryomyce 085812 streptococc 043974 leighmania Q917H1 streptococc Q8i88 trypanosoma P89597 human immun Q25297 leighmania Q25298 leighmania Q25298 leighmania Q6rv15 leighmania Aar84616 leighmania Aar84616 leighmania Q6nk47 corynebacte Cae48695 corynebacte Q36736 leighmania
QGBWUG 085812 091374 Q9RHP1 Q91888 P89597 K11B LEIIN KN11_LEITR CGRV15 AAR84616 GGRV47 CAE48695
0000000000000
1001 1005 78 78 78 78 78 78 78 78 78 78 78 78 78 7
100.55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
666 665 665 6665 6665 6665 66665
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

## ALIGNMENTS

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AND SEQUENCE FROM N.A.

MEDILINE-9098454; PubMed=9883985;

MEDILINE-9098454; PubMed=9883985;

R. Robertson J.A., Bhattacharyya S., Ing N.H.;

R. Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and standarden up-regulates oestrogen seceptor-alpha, c-fos and glyceraldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";

R. Steroid Biochem. Mol. Biol. 67:285-292(1998).

B. Mansylad AAB578401; -.

GO; GO:0008576; Cextracellular; IEA.

GO; GO:000859; P:lipid binding; IEA.

GO; GO:000869; P:lipid transport; IEA.

GO; GO:004315; P:lipoprotein metabolism; IEA.

InterPro; IPR000074; Apolipoprotein.

R. InterPro; PR000074; Apoliporotein.

P. Fam; PF01442; Apolipoprotein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 IDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LDNWDSLASTLSKVREQLGPVTQEFWDNLEKETASLRQEMHKDLEEARQKVQPYLD 56
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein Al (Fragment).
Ovis aries (Sheep).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.1%; Score 247; DB 2; Length 56
82.1%; Pred. No. 1.4e-12;
ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
6617 MW; 2AB38E08F1E8F1BC CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Apolipoprotein Al homolog protein (Fragment).
 56 AA.
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 PRT;
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PRELIMINARY;
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56
56 AA;
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 002762
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Matches
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MEDLINE=91369902; PubMed=1909888;
Akerlof E., Jornvall H., Slotte H., Pousette A.;
Akerlof E., Jornvall H., Slotte H., Pousette A.;
Identification of apolipoprotein Al and immunoglobulin as components of a serum complex that mediates activation of human sperm motility.";
Biochemistry 30:8986-8990(1991).
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000589; P:lipid transport; IEA.
GO; GO:0042157; P:lipid transport; IEA.
GO; GO:004157; P:lipid transport; IEA.
InterPro; IPR00074; Apolipoprotein.
InterPro; IPR009074; Apolipop. A E C3.
Pfam; PF01442; Apolipop.tein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Sperm activating protein subunit I, apolipoprotein A1, SPAP subunit I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Apollyoprotein A1 (Fragment).
Anser anser (domestic goose).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                   24625C65CBFFEDD8 CRC64;
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                     Mamm. Genome 7:509-517(1996).

EMBL; F14658; CAA2328-1; -.

GO; GO:0005276; C:extracellular; IEA.

GO; GO:0006289; F:lipid binding; IEA.

GO; GO:0006869; P:lipid transport; IEA.

GO; GO:0043157; P:lipid transport; IEA.

InterPro; IPR000074; Apolipoprotein metabolism; IEA.

InterPro; IPR009074; Apolipo A E C3.

Pfam; PF01442; Apolipoprotein; 1.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                     82 82
82 AA; 9168 MW;
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nes 41; Conservative
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                                                                                 MEDLINE=96062440; PubMed=7488287;
Merrill J.T., Rivkin B., Shen C., Lahita R.G.;
"Selection of a gene for apolipoprotein Al using autoantibodies from patient with systemic lupus erythematosus.";
Arthritis Rheum. 38:1655-1659(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIJIRE-966240; PubMeds-7488287;
MEDIJIRE-966240; PubMeds-7488287;
METAILL J.T., Shukin B., Shen C., Lahita R.G.;
"Selection of a gene for apolipoprotein Al using autoantibodies from patient with systemic lupus erythematosus.";
Arthritis Rheum. 38:165-1659(1995).
EMBL; S80442; AAB35539:1; -.
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MEDLINE=96327607; PubMed=8672129;
Winteroe A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DFWDNLEKETDWVRQEMNKDLEEVKQKVQPYLDEFQKKWKEDVELYRQKV
                                                                                                                                                                                                                                                                                                                                                                                                    Score 226; DB 2; Length 79;
Pred. No. 1e-10;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 226; DB 2; Length 79;
Pred. No. 1e-10;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                     79 79 79 79 79 79 AA; 33CA72DA854A150A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 AA; 9583 MW; 33CA72DA854A150A CRC64;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,

Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,

NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q29248;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Apolipoprotein Al homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA
                                                                                                                                                                                                                          EMBL; S80442; AAB35539.1; ...
InterPro; IPR09074; Apolipo_A_E_C3.
Lipoprotein. 79 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 35.8%;
1 Similarity 80.0%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                      SEQUENCE FROM N.A
NCBI_TaxID=10095;
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AAB35539;
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RESULT 4

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NCBI_TaxID=10118;
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Q28502;
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                                                                                090V04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APE_MACMU
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                                                                                                              DDR REAR READER OF THE PROPERTY OF THE PROPERT
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Biochemistry 15:1928-1933(1976).
-!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).
-!- SUBCELIGIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr., "Characterization of the plasma lipoproteins and apoproteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Erythrocebus.
                                                                                              MEDLINE=96128192; PubMed=8536707; MEDLINE=96128192; PubMed=8536707; Memaier D., Sellier N., Rousselot-Pailley D., Forgez P.; "Characterization of apolipoprotelin B-100, AI and C from plasma lipoprotein in the goose, Anser anser. Evidence for a genetic polymorphism in ApoC-11ke apolipoproteins."; Bur. J. Blochem. 234:586-591(1995). PIR: 867972; 867972. PIR: 67972; 67972. GO: 00005576; C:extracellular; IEA. GO: 00005869; F:lipid binding; IEA. GO: 000041879; P:lipid binding; IEA. GO: 000041879; P:lipid transport; IEA.
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  Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the apolipoprotein Al/A4/E family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106; DB 2; Length 34; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 1; Length 20;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, A05313; A05313.
InterPro, IPR009074; Apolipo A E C3.
Cholesterol metabolism; Direct protein sequencing; HDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brythrocebus patas (Red guenon) (Cercopithecus patas)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4BE7DFA02BF1DE91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AA; 2387 MW; 9C970997C7FC976A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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DEPQAPLDRLKDLVDVYLETVKASGKDYLAQFE 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
02-ULJ-2004 (Rel. 44, Last annotation update)
Apolipoprotein A-I (Apo-AI) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo_A_E_C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=76184721; PubMed=178359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DEPPQSPWDRVKDLATVYVD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01442; Apolipoprotein;
SEQUENCE 34 AA; 3838 MW; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%;
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chylomicrons.
                           WCBI_TaxID=8843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9538
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                                                                                                     Rattus sp. .
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] __SEQUENCE FROM N.A.
MEDLINES-96225955; PubMed-8635577;
Morelli L., Wei L., Amorim A., McDermid J., Abee C.R., Frangione B., Walker L.C., Levy E.;
"Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                         4A0103DCB6242BF3 CRC64;
                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                      SEQUENCE.
MEDLINE=9535312; PubMed=7629028;
Motojima K., Goto S.; Goto Go: 0008289; Filpid binding; IEA.
GO; GO: 0008289; Filpid binding; IEA.
GO; GO: 0041157; Pilpid transport; IEA.
GO; GO: 0041157; Pilpid transport; IEA.
InterPro; IPROGOOT4; Apolipoprotein.
Pfam; PF01442; Apolipoprotein; 1.
SEQUENCE 30 AA; 3355 MW; 4A0103DCB6242BF3 CR(
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8
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Last annotation update)
30 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 POSPWDRVKDLATVYVDVLKDSGRDYVS 31
                                   Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apolipoprotein E (Apo-E) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seqn
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                              16.08;
67.98;
                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-CT-2003 (TrEMBLrel. 25, Apolipoprotein E (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 67.95
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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NON TER
SEQUENCE
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                                                                                                                                                           Query Match
                                                                                                                                                                       Local
                                                              DOMAIN
REPEAT
                                                    DOMAIN
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REPEAT
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                                                                                                        REPEAT
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                                                                                                                                                                                                                                             58 SKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEBVKAKVQPYLDDFQKKWQEEMELYRQ 117
                                                                                                                                                                                                                                                         25 SELEEQLSPVAEETRARLSKELQAAQARLGADMEDVRSRLVQYRSEVQAMLGGSTEELRA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=9622595; PubMed=8635577;
MEDLINE=9622595; PubMed=8635577;
MOTETIL L., Wei L., Amorim A., McDermid J., Abee C.R., Frangione B., Walker L.C., Levy E.;
"Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys: apolipoprotein B genotype.";
PEBS Lett. 379:132-134(1996).";
PEBS Lett. 379:132-134(1996).";
Ilipoprotein particles. It can serve as a ligand for the LDL (apo B/E) receptor and for the specific apo-E receptor (chylomicron B/E).
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Saimiri ediureus (Common squirrel monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Cebinae, Saimiri.
                                                                                  LDL receptor binding (Potential).
Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
                 InterPro; IPR00074; Apolipoprotein.
InterPro; IPR009074; Apolipo_A_E_C3.
Pfam; PF01442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 107;
                                                                                                                                                                                                                          29; Indels
                                                                                                                                                                                12382 MW; E1D38C32F5AACB23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                107 AA
                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch }.
                                                                                                                                                                                                     13.5%; Score 85; 29.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02649; 1NFN.
InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo_A_E_G3.
                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein E (Apo-E) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                PRT;
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15-DEC-1998 (Rel. 37, Last seq
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                                                                                                                                                                                                    Query Match 13.5
Best Local Similarity 29.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                              Plasma; Repeat; VLDL.
                                                                                                                                                                                107 AA;
           HSSP; P02649; 1NFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9521;
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85 RL 86
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Runst F., Ogsawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Ra Parriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Buruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Ra Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Ra Endison E.K., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Ra Entian K.-D., Errington J., Fabret C., Ferrari B., Foulger D.,
Ra Entian K.-D., Fulita M., Pulita Y., Fuma S., Galizzi A., Galleron N.,
Rhibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
Jones L.-M., Joris B., Karamata D., Kashara Y., Klaerr-Blanchard M.,
R. Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Mchano M., Kurita R., Lapidus A., Liu H., Masuda S., Mauel C.,
RA Mchano M., Kurita R., Lepidus A., Liu H., Masuda S., Mauel C.,
RA Roback M., Noone D., O'Reilly M., Ogswa K., Ogswara A., Oudega B.,
RA Rescott A.M., Presecan B., Pulic P., Purmelle B., Rapoport G.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
Schfone R., Sato T., Scanlan E., Schleich S., Schroeter R.,
Schfone R., Sato T., Scanlan E., Schleich S., Schroeter R.,
Schfone R., Takeuchi M., Tamakoshi A., Taraka T., Tarkahashi H.,
Rasarootti A., Viari A., Wambutt R., Wambute R.,
Rasarootti A., Viari A., Wambutt R., Wedler E., Wedler H.,
Rasumotto K., Yata K., Yoshida K., Yamamoto H., Yamane K.,
Rasumoto K., Yata K., Yoshida K., Yamaneten R.,
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                                                                                                                                                  LDL receptor binding (Potential).
Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
Pfam; PF01442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
Plasma; Repeat; VLDL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 SELEEQLSPVAEETRARLSKELQAAQARLGADMEDVRSRLAQYRSEVQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 107; 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLREGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA; 12328 MW; FF88CED47BD18F7C CRC64;
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Bacillus subtilis.
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Name=yhjA; OrderedLocusNames=LL0783;
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Les 27; Conserv
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                                                                                                                                    NCBI_TaxID=1360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 GKOLNIKILDNWDSVTSTPSKIREQLGPVTQEFWDNLEKETEGIR--QEMSKDLEEVKAK 96
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                                          "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                     Complete proteome; Hypothetical protein.
SEQUENCE 118 AA; 13066 MW; 0F599F7011DD7F46 CRC64;
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1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical cytosolic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 DNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKK 107
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.8%; Score 81; DB 2
Best Local Similarity 26.2%; Pred. No. 56;
Matches 22; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 AA.
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                                                                                                                                                     Hypothetical protein yhjA.
    Yoshikawa H., Danchin A.;
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                                                                                                                           Nature 390:249-256(1997)
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Best Local Similarity
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01-JUN-2001
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                                                                                                                                   SNON protein (Fragments).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=93293901; PubMed=8514802;
Nagase T., Nomura N., Ishii S.;
"Complex formation between proteins encoded by the ski gene family.";
J. Biol. Chem. 268:13710-13716(1993).
PIR; B46598; B46598.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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12.1%; Score 76.5; DB 2; Length 7
Best Local Similarity 29.1%; Pred. No. 82;
Matches 23; Conservative 16; Mismatches 37; Indels
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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Search completed: December 21, 2004, 13:34:43 Job time : 192 secs

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December 21, 2004, 13:20:25; Search time 157 Seconds (without alignments) 274.188 Million cell updates/sec
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631
1 DEPPQSPWDRVKDLATVYVD......LDDFQKKWQEEMELYRQKVE 120
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GenCore version 5.1.6 'Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2002s;* geneseqp2003as;* geneseqp2003bs;* geneseqp2004s;* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*

A_Geneseq_23Sep04:*

Database

SUMMARIES

* Query e Match Length DB ID Description	5 75.5 120 4 AAU30469 Aau30469 Aau30469 Aau30469 Aau30469 Aau30469	75.5 120 4 AAU30267 Aau30267 Novel	65.0 119 4 AAU30468 Aau30468 Novel	31.2 65 6 ABP76131 Abp76131 Human	30.6 42 2 AAR20164	25.7 64 5 ABP31744 Auman a	21.9 32 2 AAR20165 Aar20165	21.7 26 7 ADE76474 ApoAI G	19.5 85 8 ADP87441 Adp87441	18.9 85 8 ADP87442 Human e	18.9 85 8 ADP87440 Adp87440	18.7 22 1 AAP92072 Apolipo	18.4 21 1 AAP90956 Aap90956	17.1 84 2 AAY42554 Aay42554	17.0 85 8 ADP87439 Adp87439	16.5 26 4 AAG62609 Apol	16.1 107 8 ADP87432 Adp87432	16.1 107 8 ADP87431 Adp87431 Rat	16.0 85 8 ADP87438 Adp87438 Chic	15.4 19 1 AAP92073	5 15.3 95 6 ABP70773 Abp70773	4 14.9 30 7 ADC29665	14.9 3	
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222288888888844 678801284367880011	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

### ALIGNMENTS

RESULT 1

Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia. AAU30469 standard; protein; 120 AA Novel human secreted protein #960. Tang YT, Liu C, Drmanac RT; 16-APR-2001; 2001WO-US008656. 18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160. (first entry) (HYSE-) HYSEQ INC. WO200179449-A2. Homo sapiens. 18-DEC-2001 25-OCT-2001. AAU30469; AAU30469 

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy. WPI; 2001-611725/70.

Claim 20; Page 297; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells for use in treatment of a pathology related to aberrant expression to proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell

secreted proteins of the invention

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon subliferation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human
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proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33104 represent the amino acid sequences of novel human secreted proteins of the invention
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                                                                                                                                                                                                                                                          DEPPQSPWDRVKDLATVYVDVLKDSGK--------DSVTSTFSKL 61
                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                DB 4; Length 120;
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0
                                                                                                                                                Score 476.5; DB 4
Pred. No. 2.7e-36;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein #758.
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Best Local Similarity 79./v
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                                                                                                                Sequence 120 AA;
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon a cimination, as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-ANU33304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                    REQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMBLYRQK 118
                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                      25 DEPPOSPWDRVKDLATVYVDVLKDSGK----------DSVTSTFSKL
                                                                                                                                   1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                 23;
                                                               Length 120;
                                                                                                 Indels
                                                                   DB 4;
                                                               Score 476.5; DB 4
Pred. No. 2.7e-36;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                         AAU30468 standard; protein; 119 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #959.
                                                                 75.5%;
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                                                                                                   Conservative
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                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 119 AA;
                                 Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2001.
                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                           AAU30468;
                                                                                                                                                                                                      61
                                                                 Query Match
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                           AAU30468
                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                    ઠે
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Query Match Matches

8 셤 ઠ g ABP76131;

ABP7613: RESULT

103

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The peptides represented in AAR20164-65 are capable of immunologically mimicking an Apo AI epitope. They are useful in diagnosis and detection of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is useful in therapeutic methods for increasing LCAT- mediated cholesterol esterification in humans. The Apo AI polypeptide is selected from the peptides indicated in the features and includes amino acids 13-28 defining a conserved native epitope on Apo AI capable of immunoreacting with monoclonal antibody MAB AI-11. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo Ai in vascular fluid samples and increase LCAT-mediated cholesterol esterification in humans.
                                                                                                                                                           Monoclonal antibody; MAB AI-11; epitope; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 QEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obs.; Score 193; DB 2; Local Similarity 100.0%; Pred. No. 1.3e-10; Se 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith RS;
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ε,
 AAR20164 standard; peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP31744 standard; protein; 64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 68; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonnet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00534761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCRI ) SCRIPPS CLINIC & RES
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banka CL,
                                                                      (revised)
                                                                                                                        Apo AI polypeptide (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-007201/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curtiss LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1990;
                                                                    25-MAR-2003
01-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1991
                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                      Peptide
Peptide
                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ3691) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                    43 NLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 102
                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                          Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Giordano J;
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                                     Gaps
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Score 410; DB 4; Length 119;
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J, Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                central nervous system; cardiovascular; gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 37
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                100.0%; Pred. No. 3.9e-30; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 197; DB 6; Pred. No. 9.6e-11;
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100.0%; Pred. No. >...
0; Mismatches
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                                                                                                                                                                                                                                                               ABP76131 standard; protein; 65 AA
                                                                                                                                                                                                                                                                                                                                                                       Human GENSET protein SEQ ID 457.
                                                                                                                                         DFOKKWOEEMELYROKVE 120
                                                                                                                                                               DFQKKWQEEMELYRQKVE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2001; 2001WO-IB000914
65.0%;
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Best Local Similarity 100.(
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-075548/07.
              Local Similarity
nes 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200283898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
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Gaps ö

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Human apolipoprotein-like ORF717 protein, SEQ ID NO:1434.

RESULT 5

RESULT

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Length 42; Indels Sequence 64 AA;

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Leach MD, Shimkets RA; 

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoias regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholestererol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

Homo sapiens.

WO200190366-A2

29-NOV-2001

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

WPI; 2002-106200/14. N-PSDB; ABN75770 Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 10; Page 625; 2508pp; English.

call differentiation, immune modulation, beamatopoiesis regulation, tissue growth, anglogenesis, activin or inhibin activity, chemotactic/ chemothinetic activity, heamostatic activity, tumour inhibition activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinflammatory also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, uncleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, cardiovascular diseases, immune system disorders disease, activity and protein and cholesterol ester cardiovascular diseases, immune system disorders diseases, and infections diseases caused by viral, bacterial, thungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripte, in the identification and cloning of homologous cortications any activity of ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studding the function and/or activity of ORFX protein, and in drug screening. The ORFX protein may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN7587 represent CDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and activity, and methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, Sequences ABP31028-ABP35561 represent 4534 novel human proteins

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Gaps

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94 KAKVQPYLDDFQKKWQEEMELYRQKVE 120

26; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Apo AI polypeptide(s) and anti-Apo antibodies - used to detect Apo Ai in vascular fluid samples and increase LCAT-mediated cholesterol esterification in humans.
                          Gaps
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 Score 162; DB 5; Length 64;
Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32;
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96.3%; Pred. No. 1.2e-05;
tive 0; Mismatches 1; Indels
                        6; Indels
                                                 41
                                                             Monoclonal antibody; MAB AI-14; epitope; diagnosis.
                                                 2 EPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith RS
                          Mismatches
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonnet DJ,
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                                                                                                                                                                                                                                                                                                                                                                                     /label= GLU, PHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 68; 87pp; English.
                       4 ;
                                                                                                                                  AAR20165 standard; protein; 32
25.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-00534761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00534761,
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                                                                                                                                                                                             (first entry)
                        30; Conservative
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                                                                                                                                                                                                                  Apo AI polypeptide (B)
                                                                                                                                                                                                                                                                                                     (revised)
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Best Local Similarity
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32 AA;
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                                                                                                                                                                                25-MAR-2003
01-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                            WO9118619-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-1991.
                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                         AAR20165;
                                                                         25
                                                                                                                                                                                                                                                                                                               Peptide
Peptide
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                                                                                                                                                                                                                                                                                                                                                   Peptide
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                          Matches
                                                                                                          RESULT 7
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WDRVKDLATVYVDVLKDSGRDYVSQF

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The invention relates to a novel isolated G-type polypeptide that ameliorates a symptom of atherosclerosis or other pathology associated with an inflammatory response comprising an amphipathic helical peptide having charged residues on the polar face of the peptide and possessing a wide non-polar face. The polypeptide of the invention demonstrates antiarteriosclerotic, antiinflammaticy, osteopathic, neuroprotective, dermacological, antiinflammatory, osteopathic, neuroprotective, nootropic, anti-HIV, virucide and antibacterial activities. The nootropic, anti-HIV, virucide and antibacterial activities. The ameliorating one or more symptoms of atherosclerosis and/or pathologies characterised by an inflammatory response such as rheumatoid arthritis, systemic lupus erryhematosus, polyarteritis nodesa, osteoporosis, composition and methomatosus, polyarteritis nodesa, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G-type polypeptides for preventing or ameliorating symptoms of atherosclerosis or pathologies associated with an inflammatory responses e.g. rheumatoid arthritis, osteoporosis, Alzheimer's disease, AIDS or infections.
                                                                                                                                                                                                                                                                             antiarteriosciencia, antiheumatic; antiarthritic; immunosuppressive; dermatological; antihifleumatic; antiarthritic; immunosuppressive; dermatological; antihiflammatory; osteopathic; neuroprotective; notoropic; anti-HIV; virucide; antibacterial; rheumatoid arthritis; systemic lupus erythematosus; polyarteritis nodosa; osteoporosis; Alzheimer's disease; AIDS; infection; apoAI.
                                                                                                                                                                                                                          ApoAI G* amphipathic helical domain-derived peptide - SEQ ID
                                                                                                                                                                                                                                                                 G-type; atherosclerosis; inflammatory; G* amphipathic helix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Optional N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Optional C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Optionally D-form residue"
                     27
Claim 7; SEQ ID NO 21; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .26
                                                                                                            ADE76474 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2002; 2002US-00120508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2002; 2002US-00120508
                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fogelman AM, Navab M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-831662/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003191057-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                   ADE76474;
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Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is monkey apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                            sable database system; ontology; protein analysis;
product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 SALGKOLNIKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diemer K, Guo N;
n S, Vandergriff J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.5%; Score 123; DB 8; Length 85; 31.8%; Pred. No. 0.00095; tive 23; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mi H, Dieme
Rabkin S,
                                                                                                                                                                                              Monkey apolipoprotein A (APO-A) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 48; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campbell MJ,
Muruganujan A,
        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 KVQPYLDDFQKKWQEEMELYRQKVE 120
1 WDRVKDLATVYVDVLKDSGRDYVSQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: |: :: :| :: | :: | 61 RLLPHANEVSQKIGENVRELQQRLE
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                                                                                           ADP87441 standard; protein; 85
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                                                                                                                                                              (first entry)
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Lazareva B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                             Macaca fascicularis.
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                                                                                                                                                                                                                             Browsable database
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                                                                                                                                                              09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doremieux O;
                                                                                                                                                                                                                                                                                                                                                             24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas PD,
Ladunga I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an output,
                                                                                                                             ADP87441;
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                                                                                                                                                                                                                                                                monkey.
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Matches
                                                            RESULT
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95 9

RESULT 10 ADP87442

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Gaps

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21.7%; Score 137; DB 7; I 100.0%; Pred. No. 1.1e-05; ive 0; Mismatches 0;

Length 26; Indels

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WO2004053769-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 85 AA;
                                                        Papio anubis
                                                                                                                                                                                                                               Doremieux O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
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                                                                                                         24-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                    baboon.
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                                                                                                                                                                                                                                                                                                                                                              Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analyshing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is human apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SELTQQLNALFQDKLGEVNTYAGDLQKKLVPFATELHERLAKDSEKLKEEIGKELEELRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 SALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
                                                                                           Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                         Mi H, Diemer K, Guo N;
Rabkin S, Vandergriff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a browsable database system for use with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.9%; Score 119; DB 8; Length 85; Best Local Similarity 29.4%; Pred. No. 0.0022; Matches 25; Conservative 25; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baboon apolipoprotein A (APO-A) IV precursor protein.
                                                                       Human apolipoprotein A (APO-A) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 49; 113pp; English.
                                                                                                                                                                                                                                                                                         Campbell MJ,
Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 KVQPYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: |: :: :| :: :| :: | RLLPHANEVSQXIGDNLRELQQRLE 85
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 ADP87442 standard; protein; 85 AA.
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                                                                                                                                                                                                                   09-DEC-2003; 2003WO-US038935.
                                                                                                                                                                                                                                          09-DEC-2002; 2002US-0431879P
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                                                entry)
                                                                                                                                                                                                                                                                                          Thomas PD, Kejariwal A,
                                                                                                                                                                                                                                                                                                       Lazareva B,
                                                                                                                                                                                                                                                                  (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                         WPI; 2004-480967/45.
                                               (first
                                                                                                                                                                     WO2004053769-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 85 AA;
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                  Doremieux O;
                                               09-SEP-2004
                                                                                                                                                                                            24-JUN-2004
                       ADP87442
                                                                                                                      human.
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Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is baboon apolipoprotein A (APO-A) IV precursor protein. This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 SALGKOLNIKLIDNWDSVTSTFSKIREQIGPVTQEFWDNIEKETEGIRQEMSKDIEEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mi H, Diemer K, Guo N;
Rabkin S, Vandergriff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a browsable database system for use with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL; coronary artery disease; CAD; Apo AI epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 47; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campbell MJ,
Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein AI (Apo AI) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVQPYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: |: :: :| : :| :: |
RLLPHANEVSQKIGENVRELQQRLE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
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                                                                                                                                                                                                                                                                                                                                                                            09-DEC-2003; 2003WO-US038935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-2002; 2002US-0431879P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomas PD, Kejariwal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lazareva B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APPL-) APPLERA CORP
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Best Local Similarity
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Apo AI contains the sequence below (Claim 1 claims AAs 1-15). There is inverse correlation between plasma levels of Apo AI and coronary artery disease risk. The monoclonal antibody recognises this epitope on native Apo AI. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating conditions associated with lipid oxidation or preventing oxidation in lipid-containing food, lipid containing pharmaceuticals or cosmetic or dermatological compositions.
                                                                                                                                                                                      Apo lipoprotein peptide and monoclonal antibody against it - used to assay peptide in vascular fluid to identify risk of coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholesterol; cardiovascular disease; heart disease; atherosclerosis; lipoprotein; angina; myocardial infarction; stroke; thrombosis; antioxidant; hypolipidaemic; apolipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apolipoprotein A-IV derived lipid oxidation suppressant peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 1; Length 21; Pred. No. 0.00075; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                ch 18.4%; Score 116; Di
1 Similarity 100.0%; Pred. No. 0.(
21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                (SCRI ) SCRIPPS CLINIC & RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42554 standard; peptide; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEPPOSPWDRVKDLATVYVDV 21
                                                                                                                                                                                                                                                  Claim 2; Page 41; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             DEPPQSPWDRVKDLATVYVDV
                                         89WO-US001262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US006580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                             Smith RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-580739/49.
                                                                                                                                                           WPI; 1989-309644/42.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                         27-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-1999
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                                                                      29-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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             05-0CT-1989
                                                                                                                               Curtiss LK,
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI90-111 and smaller peptides contained within this sequence. AI95-105, AI190-105 and AI190-111 are specifically claimed. Such Apo AI peptides are capable of immunologically mimicking a native conserved Apo AI epitope. They may be helpful in the diagnosis of risk of coronary heart disease. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monoclonal antibody and polypeptide antigens - directed against APO AI-HDL epitope, useful in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 100.0%; Pred. No. 0.(
22; Conservative 0; Mismatches
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 LEEVKAKVQPYLDDFQKKWQEE 111
                                                                                                                                                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS CLINIC & RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Table 1-2; 62pp; English.
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                                                                                                                                                                                                                                12. .22
/label= AI101-111
                                                                                                                                                                                                                   AI100-105
                          . . 22
|abel= A190-111
                                                                     AI90-111
                                                                                                AI90-105
                                                                                                                             AI93-101
                                                                                                                                                           AI95-105
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                                                                                                                4. .12
/label= ;
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/label= ,
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/label= .
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/label=
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label=
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label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apo AI epitope
                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1987;
                                                                                                                                                                                                                                                                                                                                      02-NOV-1988;
                                                                                                                                                                                                                                                                           WO8904486-A.
                                                                                                                                                                                                                                                                                                         18-MAY-1989
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19-FEB-1990
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            Key
Peptide
                                                       Peptide
                                                                                 Peptide
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                                                                                                                                           Peptide
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This sequence represents a peptide (#2) derived from apolipoprotein (apo)
A-IV with lipid oxidation inhibitory activity. Lipid oxidation plays a
role in the development of atherosclerosis, a main cause of coronary
chart disease. Atherosclerosis is thought to begin with local injury to
the arterial endothelium, followed by proliferation of arterial smooth
cuscle cells, along with deposition of lipid and accumulation of foam
cells in the lesion. As the atherosclerotic plaque develops, it
progressively occludes more and more blood vessel and can eventually lead
cells in the lesion. Both the plasma concentration and qualitative
characteristics of low density lipoproteins (LDL) are risk factors in
atherogenesis. Oxidation causes important changes in the primary
controlled the main LDL apolipoprotein BLOD are risk factors in
atherogenesis. Oxidation ouses important changes in the primary
controlled the main LDL apolipoprotein by macrophages, causes the
intracellular accumulation of esters of cholesterol and the formation of
foam cells, with subsequent development of the atherosclerotic plaque.
The apo A-IV derived peptides can be used for inhibiting lipid oxidation.
The peptides can be used for treating conditions associated with lipid
oxidation. For example, they can be used for treating or inhibiting the
confaction in lipid-containing foods, lipid-containing pharmaceuticals or
cosmetic or dermatological compositions. As these peptides comprise or
imminicant it would be used for treating the humans of imminicals or
imminicant of the native apo A-IV protein the humans adminibuted to humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenicity problems with their administration to humans
                                 Claim 4; Page 53; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 84 AA;
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8 WDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGFV 67 8; Gaps 17.1%; Score 108; DB 2; Length 84; 27.8%; Pred. No. 0.023; Live 22; Mismatches 35; Indels 68 TOEFWDNLEKETEGLROEMSKDLEEVKAKV 97 Best Local Similarity 27.8% Matches 25; Conservative Query Match 셤 ð 셤 ò

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Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                        Pig apolipoprotein A (APO-A) IV precursor protein.
              ADP87439 standard; protein; 85 AA
                                          09-SEP-2004 (first entry)
                                                                                                                    WO2004053769-A2.
                                                                                                      Sus scrofa.
RESULT 15
                                                                                       pig.
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Mi H, Diemer K, Guo N; Rabkin S, Vandergriff J; Campbell MJ, Muruganujan A, 09-DEC-2003; 2003WO-US038935. 09-DEC-2002; 2002US-0431879P Kejariwal A, Lazareva B, (APPL-) APPLERA CORP. Doremieux O; 24-JUN-2004 Thomas PD, Ladunga I,

WPI; 2004-480967/45

methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is pig apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention. Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and The invention relates to a browsable database system for use with Disclosure; SEQ ID NO 46; 113pp; English 

17.0%; Score 107; DB 8; Length 85; 27.4%; Pred. No. 0.029; tive 25; Mismatches 36; Indels 23; Conservative Query Match Best Local Similarity Sequence 85 AA; Matches

36 SALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA

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Gaps

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96 KVQPYLDDFQKKWQEEMELYRQKV 119 :: |: : : |: : : |:: 61 RLLPHATEVSQKIGDNVRELQQRL ò

Search completed: December 21, 2004, 13:37:26 Job time : 159 secs

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December 21, 2004, 12:34:05; Search time 142 Seconds (without alignments) 302.396 Million cell updates/sec
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631
1 DEPPQSPWDRVKDLATVYVD......LDDFQKKWQEEMELYRQKVE 120
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4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBGOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 120
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Perfect score:
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                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Sequence 403, App Sequence 405, App Sequence 276814, Description Sequence Seq US-10-038-854-403 US-10-038-854-405 US-10-424-599-276814 US-10-465-788A-89 US-10-465-788A-134 US-10-120-508-21 US-10-1465-789A-52 US-10-465-789A-50 US-10-487-096-2 US-10-487-096-2 US-10-487-096-2 US-10-4147-238A-41 US-10-142-238A-41 US-10-142-238A-41 DB Length % Query Match 1 61.4 36.0 36.0 225.7 221.7 119.3 118.7 115.3 114.9 Score 387.5 387.5 318 227 227 1162 1122 1123 1129 6.5 944 Result No.

89, Appl 1434, Ap 21, Appl 52, Appl 50, Appl 40, Appl 41, Appl 33, Appl

Sequence 37, Appl Sequence 43, Appl Sequence 43, Appl Sequence 44, Appl Sequence 35, Appl Sequence 35, Appl Sequence 46, Appl Sequence 46, Appl Sequence 47, Appl Sequence 37, Appl Sequence 224, Appl Sequence 224, Appl Sequence 224, Appl Sequence 67, Appl Sequence 13, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence	ng Same
US-10-700-340-37 US-10-142-238A-39 US-10-142-238A-43 US-10-142-238A-44 US-10-142-238A-42 US-10-142-238A-44 US-10-142-238A-44 US-10-142-238A-44 US-10-142-238A-44 US-10-142-238A-44 US-10-142-238A-34 US-10-142-238A-34 US-10-142-238A-34 US-10-142-238A-34 US-10-142-238A-36 US-10-142-238A-36 US-10-142-238A-36 US-10-142-238A-36 US-10-142-238A-36 US-10-148-231 US-10-038-854-231 US-10-038-854-231 US-10-601-100-43 US-10-601-100-43 US-10-76-701-61738 US-10-76-701-61738 US-10-601-100-36 US-10-601-100-36 US-10-601-100-36 US-10-61-100-36 US-10-61-100-36 US-10-61-100-36 US-10-61-100-36 US-10-76-701-58043 US-10-76-70-10-38 US-10-76-70-10-38 US-10-76-70-10-38 US-10-76-701-58043 US-10-76-70-10-38	ALIGNMENTS  US/10038854  11y A  R  R  R  In an and a b b b b b b b b b b b b b b b b b b
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444888888888888888888888888888888888888	403 No. US20040 No. US20040 Spytek, Kin Lii, Li, Wolenc, Ac Eisen, And Liu, Xiaol Malyakar, Shawketa, Re Rekuda, Re Patturajar Gorman, Re Gorman, Re Gorman, Re Restelli, Gangolli, Gangolli, Gangolli, Gangolli, Gangolli, Gangolli, Gangolli, Mallet, Mallet
66 67 67 67 67 67 67 67 67 67 67 67 67 6	SULT 1 Sequence 403, Application No. US20 GENERAL INFORMATION APPLICANT: Di, Li APPLICANT: Wolenc, APPLICANT: Wolenc, APPLICANT: Wolenc, APPLICANT: Eisen, APPLICANT: Gadern APPLICANT: Spimket APPLICANT: Spimket APPLICANT: Gangor) APPLICANT: Gangor) APPLICANT: Gangor) APPLICANT: Rastell APPLICANT: Burgees APPLICANT: Burgees APPLICANT: Eilerma APPLICANT: Eilerma APPLICANT: Eilerma APPLICANT: Eilerma APPLICANT: Eilerma APPLICANT: Eilerma APPLICANT: MAIDEY APPLICANT: Eilerma APPLICANT: MAIDEY APPL
1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 Sequence 403 Publication GENERAL INFO APPLICANT: APPLICAN

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MacDougall, John R
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          PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PILING DATE: 2001-04-25
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Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
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Edinger, Shlomit R
Ellerman, Karen
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Wernet, Corine
APPLICANT: Bisen, Andrew J
APPLICANT: Liu, Xiaohong
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Guo, Xiaojia S
Guo, Xiaojia S
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Smithson, Glennda
Millet, Isabelle
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; ORGANISM: Homo sapiens
US-10-038-854-403
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(351223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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US-10-424-599-276814
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98.4%; Pred. No. 5.5e-22;
tive 0; Mismatches 1;
                                             FILE REFERENCE: ALGUGA-6.20
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR PLICATION NUMBER: 60/259,785
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-02-20
PRIOR PLING DATE: 2001-02-20
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-04-29
PRIOR PLING DATE: 2001-04-13
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SEQ ID NO 276814
LENGTH: 86
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Best Local Similarity 98.4
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-10-424-599-276814
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                                                                                                                                                                                                                                                                                                      APPLICANT: FOGELMAN, ALAN
APPLICANT: FOGELMAN, ALAN
APPLICANT: NAVAB, MOHAWAD
TITLE OF INVENTION G-TYPE PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 4077-301100US
CURRENT APPLICATION NUMBER: US/10/120,508
NUMBER OF FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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                                    2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ 41
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100.0%; Pred. No. 0.00016;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
21.7%; Score 137; DB 14;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 52, Application US/10465789A
Publication No. US20040053384A1
GENERAL INFORMATION:
APPLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy H
APPLICANT: Gehuler, Mary A
APPLICANT: Gehuler, Mary A
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Welena V. Grinkova
APPLICANT: Welena V. Grinkova
APPLICANT: Welena V. Grinkova
APPLICANT: Welena V. Grinkova
APPLICANT: ON DATE: 2003-06-18
FILE REFERENCE: 87-00A
CURRENT PLILING DATE: 2003-06-18
PRIOR PILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR PILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 52
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WDRVKDLATVYVDVLKDSGRDYVSQF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic D peptide. US-10-120-508-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 WDRVKDLATVYVDVLKDSGRDYVSQF 33
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                                                                                                                                                                                                                 ; Sequence 21, Application US/10120508
; Publication No. US20030191057A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                      RESULT 6
US-10-120-508-21
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LENGTH: 26
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Publication No. US20040009474A1
Publication No. US20040009474A1
APPLICANT: INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encc FILE REFRENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 9068
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                              DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVDSTFSKL 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 162; DB 11; Length 64;
Pred. No. 1.2e-07;
4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                             US-10-465-789A-89

Sequence 89, Application US/10465789A

Publication No. US20040053384A1

GENERAL INFORMATION:

APPLICANT: Sligar, Stephen G

APPLICANT: Bayburt, Timothy H

APPLICANT: Schuler, Mary A

APPLICANT: Yelena V. Grinkova

APPLICANT: Tila G. Denisov

TITLE OF INVENTION: Membrane Scaffold Proteins

FILE REFERENCE: 87-00A

CURRENT APPLICATION NUMBER: US/10/465,789A

CURRENT APPLICATION NUMBER: 09/990,087

PRIOR APPLICATION NUMBER: 09/990,087

PRIOR APPLICATION NUMBER: 00/252,233

PRIOR PLING DATE: 2001-11-20

PRIOR FILING DATE: 2000-11-20

NUMBER: OF SEQ ID NOS: 89

SOSTWARE: PATENTIN OF PATENTIN OF PRIOR PRI
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Best Local Similarity 75.0%;
Matches 30; Conservative '
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ORGANISM: Homo sapiens
                                                                                                                                                      US-09-864-408A-1434
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LENGTH: 64
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1 LKLLDNWDSVTSTFSKLREQLG 22
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ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity
Matches 23; Conserva
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Best Local Similarity
Matches 19; Conserv
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; OTHER INFORMATION: artificial sequence of Helix 2
US-10-465-789A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 22; Conservative 0; Mismatches 0;
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US-10-465-789A-49
              NS-10-165-789A-50

Sequence 50, Application US/10465789A
Publication No. US20040053384A1
FUBLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy H
APPLICANT: Bayburt, Timothy H
APPLICANT: Civjan, Natanya R
APPLICANT: Yelena V. Grinkova
APPLICANT: Sphlar V. Grinkova
APPLICANT: Schuler, Nambrane Scaffold Proteins
TITLE REFERENCE: 87-00A
CURRENT APPLICATION NUMBER: 09/990,087
FRIOR APPLICATION NUMBER: 09/990,087
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
SOOTWARE: PatentIn version 3.1
SEQ ID NO 50
TENGTH: 22
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Publication No. US20040053384A1
GENERAL INFORMATION
APPLICANT: Sligar, Stephen G
APPLICANT: Sligar, Stephen G
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Civian, Natanya R
APPLICANT: Velena V. Grinkova
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
TITLE OF INVENTION UNMER: US/10/465,789A
CURRENT FILING DATE: 2003-66-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
PRIOR FLIING DATE: 2001-11-20
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 PVTOEFWDNLEKETEGLRQEMS 87
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Sequence 39, Application US/10142238A
Publication No. US20030087819A1
GENERAL INFORMATION:
APPLICANT'S Bislicki, John K.
TITLE OF INVENTION:
TITLE REFERENCE: 1B-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT PAPLICATION NUMBER: US 60/289,944
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PAtentin version 3.1
SEQ ID NO 39
LENGTH: 30
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PRIOR APPLICATION NUMBER: PCT/GB02/02022
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: GB0110790.3
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-08-14
PRIOR PILING DATE: 2001-08-14
PRIOR PILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: GB0120045.0
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-11-22
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 37
LENGTH: 16
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ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Publication No. US20040203023A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREATITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/700,340
CURRENT FILING DATE: 2003-11-03
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US-10-142-238A-33
is Sequence 33, Application US/10142238A
is Sequence 31, Application No. US20030087819A1
is GENERAL INFORMATION:
is APPLICANT: Bielicki, John K.
if TILLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
is FILE REFERENCE: IB-1705
is CURRENT FILING DATE: 2002-08-19
is PRIOR FILING DATE: 2002-08-19
is NUMBER OF SEQ ID NOS: 84
is SOFTWARE: PATENTIN VERSION 3.1
is SEQ ID NO 33
is LENGTH: 18
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                           APPLICANT: Bielicki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES FILE REPRENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT PILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR PILING DATE: 2001-05-09
RIONER PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
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14.6%; Score 92; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 94; DB 14; Length 30; 95.0%; Pred. No. 0.096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(18)
OTHER INFORMATION: HUMAN GENETIC ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 LNLKLLDNWDSVTSTFSKLR 61
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ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                    ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 95.03
Matches 19; Conservative
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NAME/KEY: PEPTIDE
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LENGTH: 30
TYPE: PRT
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Sequence Sequence

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Sequence 2, Application US/08292870

Patent No. 5814467

GENERAL INFORMATION:

APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Smith, Richard S
ITILE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
ITILE OF INVENTION: METHODS

ITILE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel

STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,870

FILING DATE: 17-40G-1994

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/534,761

FILING DATE: 06-70W-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/711,333

FILING DATE: 06-70W-1991

PRIOR APPLICATION NUMBER: PCT/US 91/04038

FILING DATE: 07-70W-1991

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163
US-08-710-749-1
US-08-867-087B-34
US-08-867-087B-34
US-09-205-258-1080
US-08-479-078-7
US-08-110-749-110
US-09-147-875A-111
US-09-147-875A-112
US-09-183-861-61
US-09-183-861-61
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US-09-555-501A-61
US-09-555-501A-61
US-09-555-501A-61
US-09-555-501A-61
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US-09-565-501A-61
US-09-565-501A-61
US-09-565-501A-61
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-09-134-000C-3703
                                        -09-205-258-1080
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TELECOMMUNICATION INFORMATION:
TELEPAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.STICS:
LENGTH: 44 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  CITY: La Jolla
STATE: California
COUNTRY: US
    99999999999999999
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US-08-292-870-2
  Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 105, Appli
Sequence 92, Appli
Sequence 92, Appli
Sequence 92, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 47, Appli
Sequence 11, Appli
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Sequence 4548, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
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                                                                                      December 21, 2004, 13:06:21; Search time 38 Seconds (without alignments) 209.425 Million cell updates/sec
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(GGTZ = 6/ptodata1/iaa/backfiles1.pep:*
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Compugen Ltd.
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US-08-392-970-5
US-08-333-577-5
US-08-333-577-5
US-08-182-175A-105
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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length: 120
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Perfect score:
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Maximum DB seq
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No.
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TOPOLOGY:
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US-08-292-870-3
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US-08-292-870-1
Sequence 1, Application US/08292870
Factor No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Bonnet, David J
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APPO AI POLYPEPTIDES, DIACNOSTIC METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                            Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8 CITY: La Jolla STATE: California
                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: U-AUG-1994
CLASSIFICATION 1436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
ATPOINT APPLICATION NUMBER: US 07/711,333
FILING DATE: 07-JUN-1991
ATPOINT APPLICATION THOMBER: 14,163
REGISTRATION NUMBER: 34,163
REBERNICE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEFRAN: 619-554-2937
THEREFAX: 619-554-2937
THEREFAX: 619-554-2937
                                                                                                                                                                                                                         83 RQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE 120
                                                                                                                                                                                                                                                  1 RQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVTE 38
                                                                                                                       Score 198; DB 2; L
Pred. No. 1.2e-12;
                                                                                                                       Query Match 31.4%; Score 198; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 92037
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 amino acids
; TOPOLOGY: linear; MOLECULE TYPE: peptide; FRAGMENT TYPE: internal US-08-292-870-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Gaps

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Sequence 3, Application US/08292870
; Sequence 3, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Banka, Carole L
; APPLICANT: Bannet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STEET: 10666 No. 5814467th Torrey Pines Road., TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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or F (Phe)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29,870
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
PILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: O7-JUN-1991
ATTONEY/AGENT INFORMATION:
ANDER CALLING DATE: PARAMATION:
ANDER CALLING DATE: PARAMATICN:
A
1 EMSKDLEEVKAKVOPYLDDFQKKWQEEMELYRQKVE 36
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Region
LOCATION: 11
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity
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Sequence 5, Application US/08333577

Batent No. 5786206

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Woung, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Witztum, Joseph L.
APPLICANT: Witztum, Joseph L.
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCES: 20
CORRESPED Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE Minnamow, Lid.
                     APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91, DB 1; Length 16;
Pred. No. 0.01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 1935
PRIOR DATE: 19921008
FILING DATE: 18-70N-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICANT: Witztum, Joseph L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 KVQPYLDDFQKKWQEE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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ZIP: 60601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-333-577-5
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                                                                                                                                                         APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bannet, David J
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APP AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: The Scrippe Research Institute, Office of ADDRESSE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION NUMBER: US/08/292,870
FILING DATE: 07-AUN-1990
PRIOR APPLICATION NUMBER: US 07/534,761
PRIOR APPLICATION NUMBER: US 07/711,333
FILING DATE: 07-JUN-1991
PRIOR APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
ATPORNEY/AGENT INFORMATION:
NAME: FILLING THE 07-JUN-1991
ATPORNEY/AGENT INFORMATION:
NAME: FILLING AT HOMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REBERENCE/DOCKET NUMBER: TSRI 210.1 DI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 15.0.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
                                                                              ; Sequence 4, Application US/08292870; Patent No. 5814467; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 amino acids
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Best Local Similarity 96.0°
Matches 24; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-07-959-946-5
                        RESULT 4
US-08-292-870-4
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Gaps

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, MOLECULE TYPE: protein PCT-US92-08634-5
     TOPOLOGY: linear
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: USA
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RL 69
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Sequence 5, Application PC/TUS9208634

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Woduri, Raju
APPLICANT: Voung, Stephen G.
APPLICANT: Voung, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Witztum, Joseph L.
APPLICANT: Witztum, Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies
CORRESPONDENCE ADDRESS:
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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14.4%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUW TYPE: FIOPDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANE: PATENTIN PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION UMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORIEY/AGENT IRFORMATION:
AMPLICATION PATENTIAL DATA:
ATTORIEY/AGENT IRFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
                                                                                APPLICATE
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 5CRF 234.0
TELECOMMUTICATION INFORMATION:
TELEPHONE: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gamson, Edward P.
REGISTATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN: (312)616-5400
TELEFAX: (312)616-5400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 KVQPYLDDFQKKWQEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-333-577-5
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58 SKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQ 117
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    Length 16;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRANE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,389
FILING DATE: 19920519
CLASSIFICATION: 435
                                                                                                                                                                                                                                    Sequence 7, Application US/07849389; Sequence 7, Application US/07849389; Sequence 7, Application US/07849389; GENERAL INFORMATION:
APPLICANT: HORNES, Erik
APPLICANT: HOLEN, Mathias
TITLE OF INVENTION: CLONING METHOD AND KIT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSE: 7
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
Score 91; DB 5;
Pred. No. 0.01;
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16787/168/DFBC
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US-08-182-175A-105
US-08-182-175A-105
; Sequence 105, Application US/08182175A
; Patent No. 555923
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen:
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAK: (703)683-4109
Query Match

Best Local Similarity 100.0%; P. Matches 16; Conservative 0;
                                                                                         96 KVQPYLDDFQKKWQEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 110 amino acids TYPE: AMINO ACID
                                                                                                                                      1 KVOPYLDDFOKKWOEE 16
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59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.0%; Score 76; DB 1; Length 107; Best Local Similarity 25.7%; Pred. No. 3.2; Matches 18; Conservative 22; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IES: FLOST LILES
COMPUTER: IES: FLOST LILE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIPICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: CURROWN>
APPLICATION NUMBER: 08/474,633
RIGHER ARBADA C. SIEGELL
REGISTRATION NUMBER: 30,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 92, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
                     MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1007 MARKET STREET
                                                                                                                                                                            CLASSIPICATION: 800
CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-
TELECHONE: 302-922-4931
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND COMPANY
                                                                                                                                                                                                                                                      30,684
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 92: SEQUENCE CHARACTERICTICS: LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. D
                                                                                                                                                                                                                                                                                                                                                                                                                                          : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 EMELYROKVE 120
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 KMKVMEEKMK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-474-633A-92
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US-08-823-771-92
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                       APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
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                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: B.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                       ZIP: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
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Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I. DU FONT DE NEMOURS AND
TITLE OF INVENTION: CHIMERIC GENES AND
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: AND THREONINE CONTENT
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: B. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acide TYPE: amino acide TYPE: amino acide TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
Sharon J. Keeler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 EMELYROKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:: :|::
67 KMKVMEEKMK 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19898
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ZIP: 1989
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59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
                                                                                                                                   99
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                                                                                                             | | : | : : | | : : | | : : | | : : | | : : | | | : : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 678361
FILE REFERENCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
FILOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PATENT. PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Patent No. 5800982
Patent No. 5800982
APPLICANT: HASEGAWA, AKIRA
APPLICANT: MAXI, NOBORU
APPLICANT: YAGI, SHINTARO
APPLICANT: XAGI, SHINTARO
APPLICANT: KASHIWAKUMA, TOMIKO
TITLE OF INVENTION: ANTICENTIC PEPTIDES FOR GROUPING
TITLE OF INVENTION: METHODS FOR ITS GROUPING THE SAME AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels 14;
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22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IE C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6681, Application US/09513999C
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 WATER STREET
   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3(CORRESPONDENCE ADDRESS: ADDRESSE: DAVID G. ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                         111 EMELYROKVE 120
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67 KMKVMEEKMK 76
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US-09-513-999C-6681
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-513-999C-6681
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LENGTH: 105
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US-08-685-764-4
   Matches
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TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: B.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STREET: DOUBLANTE LOUGH ARCH CARL
COUNTRY: USA
ZIP: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOCTWARE: Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE:
APPLICATION NUMBER: PCT/US92/06412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 KLREQLGPVTQEFW-----DNLEKETEGLRQEMSKDLEEVKA--KVQPYLDDFQKKWQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KLKEEMAKWKDEMWKLKEEMKKLEEKMKVMEEKWKKLEEKMKAMEDKWKMLEEKOMKKLEE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 76; DB 4; Length 107; 25.7%; Pred. No. 3.2; tive 22; Mismatches 22; Indels
   REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                        TELEX: 835420
; INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
CPOLCGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-08-823-771-92
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APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUSE 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
RESPERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPRA: (302) 992-4929
TELEPRA: 056400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 105, Application PC/TUS9206412 GENERAL INFORMATION:
                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS: LENGTH: 107 amir-
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25.7%;
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Best Local Similarity 25.7%
Matches 18; Conservative
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67 KMKVMEEKMK 76
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Best Local Similarity
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CLASSIFICATION:
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                                                                            internal
           protein
           MOLECULE TYPE:
FRAGMENT TYPE:
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: BINDING SITES
NUMBER OF SEQUENCES: 76
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01234
PRIOR APPLICATION NUMBER: US 08/084,542
FILING DATE: 28-UUN-1993
PRIOR APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
INFORMATION POR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acids
TYPE: ALLORY OF TABLES OF TA
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RRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/092,192

FILING DATE: 15-UUL-1993

APPLICATION NUMBER: JP 212061/92

FILING DATE: 16-UUL-1992

PRIOR APPLICATION DATA: 2

PRIOR APPLICATION NUMBER: JP 316634/92

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: JP 31643/92

PRIOR APPLICATION NUMBER: JP 104754/93

PLING DATE: 30-OCT-1992

PRIOR APPLICATION NUMBER: JP 104754/93

FILING DATE: 30-APR-1993

ATTORNEY/AGENT INFORMATION: NAME: BUCKLEY, LINDA M.

REGISTRATION NUMBER: 31003

REFERENCE/DOCKET NUMBER: 31003

REFERENCE/DOCKET NUMBER: 31003

TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,764
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GENERAL INFORMATION:
APPLICANT:
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TOPOLOGY: linear
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TOPOLOGY: linear
                                                                                                                            FILING DATE
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PCT-US94-01234-47
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MEDLINE-99998454; PubMed-9883985;

MEDLINE-99998454; PubMed-9883985;

Robertson U.A., Bhattacharyya S., Ing N.H.;

Robertson U.A., Bhattacharyya S., Ing N.H.;

Tamoxifen up-regulates cestrogen receptor-alpha, c-fos and

"Tamoxifen up-regulates and

"Tamoxifen up
            093%19 lactococcus
0908s3 gallus gall
057089 haemophilus
097hf1 streptococc
0731u4 treponema d
Aas12283 treponema
097av3 thermoplasm
084we onocrhynchu
08tyr5 methanopyru
P89588 human immun
085596 human immun
072p16 human immun
072p16 human immun
Aas52934 ashbya go
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
MCBI_TaxIb=9940;
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Last annotation update)
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Last annotation update)
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            Q93X19
Q9FSS3
YC51 HAEIN
Q9RHF1
Q73LU4
AAS12283
Q97AV3
AAS52934
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P89588
P89596
Q7ZPL6
Q6U9J3
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01-JUL-1997 (TrEMBLrel. 04, La
01-MAR-2004 (TrEMBLrel. 26, La
Apolipoprotein Al (Fragment).
Ovis aries (Sheep).
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milarity 82.1%;
Conservative 3
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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77
92
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95
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Best Local Similarity
Matches 46; Conserv
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SEQUENCE
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AC 022
DT 011
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Q6nk47 corynebacte
Cae48695 corynebac
Q54892 streptococc
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O9t851 sus scrofa
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P62499 ashbya goss
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                                                                                                 December 21, 2004, 12:24:55; Search time 191 Seconds (without alignments) 328.355 Million cell updates/sec
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                                                                                                                                                                                          1 DEPPOSPWDRVKDLATVYVD.....LEEVKAKVQPYLDDFQKKWQ 109
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Q86£03
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      1825181 seqs, 575374646 residues
                                                                                                                                                        US-09-803-918A-2_COPY_25_133
576
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Q6LD50
AAB15539
Q9UCT8
Q9PRR6
APA1 ERYPA
Q9QV04
APE SAISC
APE MACMU
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O85812
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Maximum Match 100%
Listing first 45 summaries
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Q9PXP4
Q6WHJ6
AAQ64377
Q81R54
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Q9CHE9
Q6NK47
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Q9LCR0
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                        - protein search, using
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 109
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Perfect score:
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MEDLINE=91369902; PubMed=1909888;

Akerlof E., Jornvall H., Slotte H., Pousette A.;

Akerlof E., Jornvall H., Slotte H., Pousette A.;

Identification of apolipoprotein Al and immunoglobulin as components of a serum complex that mediates activation of human sperm motility.";

Biochemistry 30:8986-8990(1991).

GO; GO:0005589; F:lipid binding; IEA.

GO; GO:0006889; F:lipid binding; IEA.

GO; GO:000889; F:lipid binding; IEA.

GO; GO:0004289; P:lipid binding; IEA.

InterPro; IPR00074; Apolipoprotein.

InterPro; IPR009074; Apolipo_A_E.G.3.
                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=96062440; PubMed=7488287;

Merrill J.T., Rivkin B., Shen C., Lahita R.G.;

"Selection of a gene for apolipoprotein Al using autoantibodies from patient with systemic lupus erythematosus.";

Arthritis Rheum. 38:1655-1659(1995).

EMBL. S80442; AAB35539.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sperm activating protein subunit I, apolipoprotein A1, SPAP subunit
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apolipoprotein AI (Fragment).
Anser anser (domestic goose).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              , Match 11.8%; Score 183; DB 2; Length 79; Local Similarity 80.0%; Pred. No. 3.8e-08; hes 32; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 141; DB 2; Length 26;
Pred. No. 3.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                         79 AA; 9583 MW; 33CA72DA854A150A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Q9UCT8
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Merrill J.T., Rivkin E., Shen C., Lahita R.G.;
"Selection of a gene for apolipoprotein Al using autoantibodies from a patient with systemic lupus erythematosus.";
Arthritis Rheum. 38:1655-1659(1995).
EMBL; S80442; AAB3539:1;
InterPro; IPR009074; Apolipo_A_E_G3.
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BEDLINE-26327607; PubMed=8672129;
Winterce A.K., Fredholm M., Davies W.;

Evaluation and characterization of a porcine small intestine CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10095,
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02-MAA-2004 (TrEMBirel. 27, Created)
02-MAR-2004 (TrEMBirel. 27, Last sequence update)
02-MAR-2004 (TrEMBirel. 27, Last annotation update)
Apolipoprotein Al homolog (Fragment).
Mus sp.
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                                                                                                                                                                                      library.";
Mamm. Genome 7:509-517(1996).
EMBL, F14889; CAR23298.1;
GO, GO:0005289; F14916 binding; IEA.
GO; GO:0006869; F:lipid binding; IEA.
GO; GO:0042157; P:lipid transport; IEA.
GO; GO:0042157; P:lipoprotein metabolism; IEA.
InterPro; IPR000074; Apolipoprotein.
Lipoprotein.
Lipoprotein.
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RESULT 3

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01-MAY-2000
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-I- SUBCELLULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr., 
"Characterization of the plasma lipoproteins and apoproteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brythrocebus patas (Red guenon) (Cercopithecus patas).
Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Cercopithecidae, Cercopithecidae, Erythrocebus.
                                                                                        plasma
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                                                                  Hermier D., Sellier N., Rousselot Pailley D., Forgez P., "Characterization of apolipoproteins B-100, AI and C from plas lipoprotein in the goose, Anser anser. Evidence for a genetic
 Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chylomicrons.
-!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
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Pred. No. 0.072;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                           Score 106; DB 2; Length 34;
                                                                                                                                                                                                                                                                                                                         6; Indels
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InterPro; IPR009074; Apolipo A E C3.
Cholesterol metabolism; Direct protein sequencing; HDL;
                                                                                                                                                                                                                                                              4BE7DFA02BF1DE91 CRC64;
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                                                                                                                                                      GO: GO:0005576; C:extracellular; IEA.
GO: GO:0008289; F:lipid binding; IEA.
GO: GO:0008889; F:lipid transport, IEA.
GO: GO:00048157; P:lipoprotein metabolism; IEA.
InterPro; IPR009074; Apolipoprotein.
InterPro; IRR089074; Apolipoprotein.
SEQUENCE 34 AA; 3838 MW; 4BE7DFA02BFIDE91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein A-I (Apo-AI) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                   1 DEPQAPLDRLKDLVDVYLETVKASGKDYLAQFE 33
                                                                                                                                                                                                                                                                                                                                                   2 EPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFE 34
                                                                                                   lipoprotein in the goose, Anser anser. Evider polymorphism in ApoC-like apolipoproteins."; Bur. J. Biochem. 234:586-591(1995). PIR; S67972; S67972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA.
                                                                                                                                                                                                                                                                                                       Pred. No. 0.05
                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                         MEDLINE=96128192; PubMed=8536707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erythrocebus patas monkey.";
Biochemistry 15:1928-1933(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=76184721; PubMed=178359;
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                                                                                                                                                                                                                                                                                            18.4%;
                                                                                                                                                                                                                                                                                                        54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                        Best Local Similarity
                NCBI_TaxID=8843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9538;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Marken Lic., Levy B.;
Marken Lic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and catabolism of
Apolipoprotein E (Fragment).
Rattus sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000074; Apolipoprotein.
Pfam; PF01442; Apolipoprotein; 1.
SEQUENCE 30 AA; 3355 MW; 4A0103DCB6242BF3 CRC64;
                                                                                                                                                                                                                                                                                       Motojima K., Goto S.;
J. Biochem. 117:597-602(1995).
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0006289; F:lipid binding; IEA.
GO; GO:0042157; P:lipid transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Apolipoprotein E (Apo-E) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.11
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saimiri sciureus (Common squirrel monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PQSPWDRVKDLATVYVDVLKDSGRDYVS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSOWDXVXDFATVÝVDAVXDSGXDÝXS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                         MEDLINE=95355312; PubMed=7629028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%;
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Matches 19; Conservative
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Gaps

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72

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DLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 DDLTGILDEVKDTVADKAKELKDEAVTKVGELK----DKATEKAGELKDKVVDKAKELK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAIN-ATCC 49256;

Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
LDL receptor binding (Potential).
Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
                                                                                                                                                                                                                                     58 SKLREQLGPVTQEFWDNLEXETEGLRQEMSKDLEEVKAKVQPYLDDFQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
NON-structural protein NS4=GROUP I HCV-specific antigen C14-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 96;
                                                                                                                                                                      14.2%; Score 82; DB 1; Length 107; 33.3%; Pred. No. 20; tive 12; Mismatches 20; Indels
                                                                                                                                                                                                                                                       25 SELEEQLSPVAEETRARLSKELQAAQARLGADMEDVRSRLVQYRSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=FNV0007;
Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Indels
                                                                                                                                            12382 MW; E1D38C32F5AACB23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AABF01000220; EAA23153.1; -.
INCENTRY OF 1PRO04238; LEA.
Pfam; PF02987; LEA 4; 1.
Hypothetical protein.
SEQUENCE 96 AA; 10436 MW; 7568787BAFE86350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 DNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | : | : : : | | : | EGAESKTSELKDKAAEKAEELKDKISEGADSLINK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 77.5; D
24.2%; Pred. No. 43;
:ive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical cytosolic protein.
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                                                                                                                                                                                                          16; Conservative
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   99
96
>107
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76
98
>107
                                                                                                                                            107 AA;
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Best Local Similarity
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Best Local Similarity
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    Fusobacterium
                                                                                                                              NON TER
SEQUENCE
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1D 0.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- FUNCTION: Mediates the binding, internalization, and catabolism olioprotein particles. It can serve as a ligand for the LDL (apo B/E) receptor and for the specific apo-E receptor (chylomicron remnant) of hepatic tissues.
-I- SUBCELLULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Secreted in plasma.
-I- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9622595; PubMed=8635577;
MEDLINE=9622595; PubMed=8635577;
Moralli L., Wei L., Amorim A., McDermid J., Abee C.R., Frangione B.,
Walker L.C., Levy E.,
"Cerebrovascular amyloidosis in squirrel monkeys and rhesus monkeys:
apolipoprotein E genotype.";
FERS Lett. 379:132-134(1996).
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                         LDL receptor binding (Potential).
Heparin-binding (By similarity).
B X 22 AA approximate tandem repeats.
1.
2.
3.
4.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipop.A B C3.
Pfam; PF01442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
   HSSP; P02649; INFN.
InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo A E C3.
Emm; PF01442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport; Plasma; Repeat; VLDL.
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                                                                                                                                                                                                                                                                                    14.4%; Score 83; DB 1; Length 107; 33.3%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                    20; Indels
                                                                                                                                                                                                                                                     12328 MW; FF88CED47BD18F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                    12; Mismatches
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    107 AA;
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Q28502;
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SEQUENCE
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PRELIMINARY;
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NCBI_TaxID=1392;
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                                          AAQ64377
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                                                                                                                                               MEDLINE=94245087; PubMed=7514558; Tanaka T., Tangin T., Tanaka S., Tanaka T., Tankin T., Tankin K., Yamaguchi K., Yagi S., Tanaka S., Hasegawa A., Ohta Y., Hatcori N., Kohara M.; Significance of specific antibody assay for genotyping of hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 DRDPEFATGCVSII---GRLHINQRAVVAPDKEVLYEAFDEMEECASRAALIEE-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 EGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage KVP40.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 2; Length 76;
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
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Miller E., Heidelberg J., Bisen J., Nelson W., Durkin A.
Feldblyum T., White O., Paulsen I., Nierman W., Lee J.,
Szczypinski B., Fraser C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller E., Lee J., Szczypinski B.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 AA; 11389 MW; 267CA4C1F2F7F44E CRC64;
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Hypothetical protein.
SEQUENCE 76 AA; 9023 MW; 873E2003C17C60C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQ---PYLDDF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::| | ::| | ::| ORIAEMLKSKIQGLLQQASKQAQDIKPAVQTSWPKVEQF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.9%; Score 74.5; DB
25.3%; Pred. No. 82;
ive 22; Mismatches
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InterPro; IPR001490; HCV NS4b.
Pfam; PF01006; HCV NS4a; 1.
PFam; PF01001; HCV NS4b; 1.
NON TER 102 102
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24.3%;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hypothetical protein.
ORFNames=KVP40.0307;
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Best Local Similarity 24.39
Matches 18, Conservative
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                                                                                                            SEQUENCE FROM N.A.
                                      MCBI_TaxID=11103;
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Q6WHJ6
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=22803260; PubMed=12923095;
Miller E., Heidelberg J., Eisen J., Nelson W., Durkin A., Ciecko A., Feldblyum T., White O., Faulsen I., Nierman W., Lee J., Szczypinski B., Fraser C.; "Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                              no RNA stage; Caudovirales; Myoviridae.
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MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%; Score 73; DB 2; Length 76; 24.3%; Pred. No. 79; ive 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miller E., Lee J., Szczypinski B.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY283928; AAQ64377.1; -.
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                                                   Last sequence update)
Last annotation update)
            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 KAKVQPYLDDFQKK 107
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02-MAR-2004 (TrEMBLrel. 02-MAR-2004 (TrEMBLrel. 02-MAR-2004 (TrEMBLrel. Hypothetical protein.
                                                                                                                                                                                                                                                              viruses,
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SEQUENCE 76 AA; 90
                                                                                                                                                                                                                   Bacteriophage KVP40
Viruses; daDNA virus
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SEQUENCE FROM N.A.
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RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., RA Fraser C.M.;
RA Fraser C.M.;
RI Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RU Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RA Brettin T.G., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., RA Brettin T.G., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., RA Hitchcock P., Vackson P., Keim P., Longmire J., Lucas S., Okinaka R., RA Hitchcock P., Vackson P., Keim P., Longmire J., Lucas S., Okinaka R., RA Hitchcock P., Vackson P., Rubin E., Tice H.;
RA Hitchcock P., Vackson P., Keim P., Longmire J., Lucas S., Okinaka R., RA Hitchcock P., Vackson P., Rabil Gensul, Gen
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December 21, 2004, 12:24:32; Search time 152 Seconds (without alignments) 257.247 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 109
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20028:* geneseqp2003a8:* geneseqp2003b8:* geneseqp20048:*

Description	Abp76131 Human GEN Abp31744 Human apo Aar20164 Apo Al po Ade76414 Apo Al ep Adp90956 Apo Al ep Adp87442 Human apo Aap92072 Apolipopr Aay42554 Apolipopr Adp87440 Baboon ap Adp87440 Baboon ap Adp87439 Pig apoli Adp87439 Pig apoli Adp87439 Ricken a Aap92073 Apolipopr Adp87439 Ricken a	S Anti S Anti S Pept S Brea B Anti A Anti S Apol
SUMMARIES	ABP76131 ABP31744 AAR20164 AAR201664 AAR201664 AAR90956 AAR90956 AAR92072 AAR92072 AAR92073 AAR92073 AAR97073 AAR97073	ADC29665 ADC29666 ADC29658 AAY27065 AAP57175 ADC29668 ADC29664 ADH35704 ADH35704
08	98911888118881488	001162111
% Query Match Length	66 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	30 30 11 30 30 11 11
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Score	1937 1622 1138 1138 1112 1112 1108 1108 1104 101 101 101 101 101 101 101 101 10	8888886784744646484848484848484848484848
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ADC29657 ADC29660 ADC29667 ADC29667 ADC29667 ADC29670 ADC	ALIGNMENTS	CO ID 457.  Tatory; nootropic therapy; GENSET; mmune disorder; cardiovascular; colo914.	Dumas Milne Edwards des and polypeptide inflammatory disea diovascular or gast pp; English. elates to novel GEN peptides (ABP75963-, eful in screening at compounds for trea! as heavy metal tox ers, and the neurom r gastrointestinal
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	in;	itry)  seg ID 4  therag  immune  immune  i; cardi  cardi  coo914	uma inf iov iov on com com gas
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	protein;	(first entry)  protein SEQ ID 4 antiinflammatory; inal; gene therap disease; immune ous system; cardi A1. 2001WO-IB000914.	asoure of the first of the firs
בייטטמממה ההממממ מייט בי	standard;	(first protein mulinfilmal; gendisease us syst.	ranaka joo Tanaka joo
	nđa	(f ant ant tina y di y di y y di o o o o o o i s ; 20	GENSET.  S, Tanak 33-075548/ 33-075548/ 33-075548/ 32-075548/ 32-075548/ 32-075548/ 32-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075548/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-075648/ 33-0
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00000000000000000000000000000000000000	••	uman GENSET ytostatic; astrointest nflammatory entral nerv omo sapiens 0200283898- 4-OCT-2002.	tin S, 2003-2003-2003-2003-2003-2003-2003-2003
00000000000000000000000000000000000000	1 197 197	XX XX XX XX Human GENSET protein SEQ XX XX XX KW Cytostatic; antiinflammat KW Gastrointestinal; gene th XW Inflammatory disease; imm KW central nervous system; ox XX Homo sapiens. XX YX XX XX YX XX XX XX XX XX XX XX XX	PA (GEST ) GENS XX YX YX YX YX XX WPI; 2003-07 XX New GENSET F PT metal toxici PT metal toxici PT metal toxici PT metal toxic ABZ36911) en CC ABZ36911) en CC ABZ36911 for en CC C abnormal GEN CC C clased disc CC discases, in CC discase

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ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and activity, and methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, hammacopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/chemokinetic activity, thrombolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ORF; open reading frame; ORPX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; disease grouth; cell differentiation; dimune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemocractic; chemokinetic; fertility; thrombolytic; tumour inhibition; bodily characteristic; fertility; cardiovascular disease; immune system disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic; antidiabetic; cytosteatic; noctropic; neuroprotective; antistatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antistyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
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  Length 65;
                                                                                                                                                                                                                                                                                                                                                                                       Human apolipoprotein-like ORF717 protein, SEQ ID NO:1434.
                                            Indels
                                                                                                                     DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 61
                                                                                           1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSA 37
ch 34.2%; Score 197; DB 6; L
1 Similarity 100.0%; Pred. No. 1.1e-11;
37; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                    ABP31744 Standard; protein; 64 AA.
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Query Match
Best Local Similarity
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receptor/ligand, antiinflammatory activity, tumour inhibition activity,
and antiinfective activity, and may also be involved in the determination
of bodily characteristics, fertility and behaviour. ORFX proteins,
cucleic acids and antibodies may be used in the treatment of cancers,
cucleic acids and antibodies may be used in the treatment of cancers,
cher proliferative disorders such as poorlasis and benign tumours,
neurological disorders such as epilepsy and Alzheimer's disease,
cardiovascular diseases, immune system disorders related to
organ transplantation, disorders of tissue growth and regeneration,
diseases such as diabetes mellitus, hypothyroidism, and cholesterol
ester getorage disease, and infections diseases caused by viral, bacterial,
ctungal and other pathogens. ORPX uncleic acids may also be used as a
source of primers and probes, in the detection of ORPX genomic sequences
cor transcripte, in the identification and cloning of homologous
cor transcripte, in the identification and cloning of homologous
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cordis may additionally be used to produce transgenic animals
which may be useful for studying the function and/or activity of ORFX
protein, and in drug screening. The ORFX proteins may also be used
immunogens to generate specific antibodies, which are useful in the
diagnosis, treatment and monitoring of ORFX-associated diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 162; DB 5; Length 64;
Pred. No. 2.8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; MAB AI-11; epitope; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ
                                                                                                                                                                                                                                                                                                                                                                                                          28.1%; Sco. 75.0%; Pred. No. 4... 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR20164 standard, peptide; 42 AA
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Best Local Similarity 75.0 Matches 30, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 64 AA;
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01-APR-1992
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Peptide
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Gaps

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with an inflammatory response comprising an amphipathic helical peptide having charged residues on the polar face of the peptide and possessing a wide non-polar face. The polypeptide of the invention demonstrates antiarteriosclerotic, antiarhumatic, antiarthritic, immunosuppressive, dermatological, antiinflammatory, osteopathic, neuroprotective, notropic, anti-HIV, virucide and antibacterial activities. The composition and methods of the invention may be useful in preventing or ameliorating one or more symptoms of atherosclerosis and/or pathologies characterised by an inflammatory response such as rheumatoid arthritis, systemic lupus exthematosus, polyarterifis nodosa, osteoporosis, Alzheimer's disease, AIDS or inflection. The current sequence is that of the apoAI G* amphipathic helical domain-derived peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo AI contains the sequence below (Claim 1 claims AAs 1-15). There is a inverse correlation between plasma levels of Apo AI and coronary artery disease risk. The monoclonal antibody recognises this epitope on native Apo AI. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo lipoprotein peptide and monoclonal antibody against it - used to assay peptide in vascular fluid to identify risk of coronary artery
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Pred. No. 2.5e-06;
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Pred. No. 0.00022;
0; Mismatches 0;
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100.0%; Pred. No. 2...
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100.0%; Pre
0; }
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAP90956 standard; peptide; 21
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Query Match

Best Local Similarity

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Best Local Similarity
                                                                                                                                                                                                                 Sequence 26 AA;
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19-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP90956;
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                                                                                                                                                  PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New G-type polypeptides for preventing or ameliorating symptoms of atherosclerosis or pathologies associated with an inflammatory responses e.g. rheumatoid arthritis, osteoporosis, Alzheimer's disease, AlDS or
                            The peptides represented in AAR20164-65 are capable of immunologically mimicking an Apo AI epitope. They are useful in diagnosis and detection of Apo AI in fluids and for preparing anti-Apo AI antibodies. It is useful in therapeutic methods for increasing LCAT- mediated cholesterol esterification in humans. The Apo AI polypeptide is selected from the peptides indicated in the features and includes amino acids 13-28 defining a conserved native epitope on Apo AI capable of immunoreacting with monoclonal antibody MAB AI-11. (Updated on 25-MAR-2003 to correct P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-type; atherosclerosis; inflammatory; G* amphipathic helix; antiarteriosclerotic; antirheumatic; antiarthritic; immunosuppressive; dermatological; antiinflammatory; osteopathic; neuroprotective; noorcropic; anti-HIV; virucide; antibacterial; rheumatoid arthritis; systemic lupus erythematosus; polyvarteritis nodosa; osteoporosis; Alzheimer's disease; AIDS; infection; apoAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated G-type polypeptide that ameliorates a symptom of atherosclerosis or other pathology associated
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ApoAI G* amphipathic helical domain-derived peptide - SEQ ID 21.
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Optional N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Optionally D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Optional C-terminal amide"
                                                                                                                                                                                                                             24.0%; Score 138; DB 2; I
100.0%; Pred. No. 3.7e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           84 QEMSKDLEEVKAKVQPYLDDFQKKWQ 109
                                                                                                                                                                                                                                                                                                               QEMSKDLEBVKAKVQPYLDDFQKKWQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; SEQ ID NO 21; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Ä
 Claim 2; Page 68; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            ADE76474 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2002; 2002US-00120508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2002; 2002US-00120508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Navab M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-831662/77.
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                              Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003191057-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV
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Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE76474;
                                                                                                                                                                                                                                                                                                                                                                                           ADE76474
                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Gaps

ADP87441;

RESULT 6

monkey

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Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is human apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 SALGKOLNIKLLDNWDSVTSTFSKIREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
                                                                                                  Broweable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 19.1%; Score 110; DB 8; Length 85; Local Similarity 31.9%; Pred. No. 0.0049; Ness 23; Conservative 20; Mismatches 29; Indels
                                                             Human apolipoprotein A (APO-A) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, SEQ ID NO 49; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Campbell MJ,
Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP92072 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                  09-DEC-2003; 2003WO-US038935.
                                                                                                                                                                                                                                                                                                                                                          09-DEC-2002; 2002US-0431879P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(revised)
(first entry)
                   09-SEP-2004 (first entry)
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Lazareva B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLLPHANEVSQK 72
                                                                                                                                                                                                                                                                                                                                                                                                   (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-480967/45.
                                                                                                                                                                                                                                 WO2004053769-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 85 AA;
                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
31-OCT-2002
10-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ladunga I,
Doremieux O;
                                                                                                                                                                                                                                                                         24-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an output
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP92072;
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                                                                                                                                                  human.
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ID AAP
XX AX
AX AX
DT 25-I
DT 31-I
DT 10-XX
XX APO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is monkey apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 SALGKOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                     Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mi H, Diemer K, Guo N;
Rabkin S, Vandergriff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.4%; Score 112; DB 8; Length 85; 33.3%; Pred. No. 0.0031; ive 19; Mismatches 29; Indels
                                                                                                                                                                                                           Monkey apolipoprotein A (APO-A) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, SEQ ID NO 48; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campbell MJ,
Muruganujan A,
                                                                                 ADP87441 standard; protein; 85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-2003; 2003WO-US038935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-2002; 2002US-0431879P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.33
Best Local Similarity
Conservative
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 KVQPYLDDFQKK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLLPHANEVSQK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kejariwal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazareva B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-480967/45.
                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ladunga I, ]
Doremieux O;
                                                                                                                                                                    09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas PD,
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output.

Diemer K, Guo N; 1 S, Vandergriff J;

Mi H, Diem Rabkin S,

9

Apolipoprotein AI (Apo AI) polypeptide.

ADP87442 standard; protein; 85 AA.

RESULT 7 ADP87442

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ADP87442

Gaps

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This sequence represents a peptide (#2) derived from apolipoprotein (apo)
A-IV with lipid oxidation inhibitory activity. Lipid oxidation plays a
Cotal in the development of atherosclerosis, a main cause of coronary
cotal in the development of atherosclerosis, and accumulation of foam
cells along with deposition of lipid and accumulation of foam
cells in the lesion. As the atherosclerotic plaque develops, it
progressively occludes more and more blood vessel and can eventually lead
colls in the lesion. Both the plasma concentration and qualitative
corporateristics of low density lipoproteins (LDD) are risk factors in
charcogenesis. Oxidation causes important changes in the primary
corporates of the main LDL apolipoprotein, apolipoprotein B100 (apo B-
corporate) with subsequent development of the atheroschaege, causes the
cintracellular accumulation of esters of cholesterol and the formation of
contracellular accumulation of esters of cholesterol and the formation of
contracellular accumulation of esters of cholesterol and the formation of
contracellular accumulation of esters of cholesterol and the formation of
contracellular accumulation of esters of cholesterol and the formation of
contracellular accumulation of esters of cholesterol and the formation of
contraction. For example, they can be used for treating or inhibiting the
progression of atherosclerosis. They can also be used for preventing
contaction in lipid-containing foods, lipid-containing pharmaceuticals or
cosmetic or dermatological compositions. As these peptides comprise
commetic or dermatological administration to humans
communicative problems with their administration to humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 WD-----YFTQLSNNAKEAVEQLQKTDVTQQLNTLFQDKLGNINTYADDLQNKLVPF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating conditions associated with lipid oxidation or preventing oxidation in lipid-containing food, lipid containing pharmaceuticals or cosmetic or dermatological compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 WDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 108; DB 2; Length 84; 27.8%; Pred. No. 0.0076; ive 22; Mismatches 35; Indels
                                                                                                                                                /note= "Optionally has a C-terminal amide"
  antioxidant; hypolipidaemic; apolipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : :| || || :|:|: ||: ||: ||: || || 54 AVQLSGHLTKETERVREBIQKELEDLRAMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TOEFWDNLEKETEGLROEMSKDLEEVKAKV
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP87440 standard; protein; 85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 53; 73pp; English.
                                                                                                                                                                                                                                                                          99WO-US006580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.8*
Best Local Similarity 27.8*
                                                                                                                                                                                                                                                                                                                                                              (UYCI-) UNIV CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-580739/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 84 AA;
                                                                                                           Key
Modified-site
                                                                                                                                                                                          WO9950286-A2
                                                                                                                                                                                                                                                                             25-MAR-1999;
                                                                                                                                                                                                                                                                                                                    31-MAR-1998;
                                                             Hômo sapiens
                                                                                                                                                                                                                                     07-0CT-1999
                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP87440;
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  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI190-105 and AI190-11 are specifically claimed. Such Apo AI peptides are capable of immunologically mimicking a native conserved Apo AI epitope. They may be helpful in the diagnosis of risk of coronary heart disease. (Updated on 31-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New monoclonal antibody and polypeptide antigens - directed against APO AI-HDL epitope, useful in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI90-111 and smaller peptides contained within this sequence. AI95-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholesterol; cardiovascular disease; heart disease; atherosclerosis; lipoprotein; angina; myocardial infarction; stroke; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein A-IV derived lipid oxidation suppressant peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108; DB 1; Length 22
Pred. No. 0.0014;
Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL;
coronary artery disease; CAD; Apo AI epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.8%; Score 108; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCRI ) SCRIPPS CLINIC & RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Table 1-2; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         12. .22
/label= AI101-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42554 standard; peptide; 84 AA
                                                                                                                                                                                                                                                                                                                                                                                                     A1100-105
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                                                                                                                                                                                                               . .16
label= AI90-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEVKAKVQPYLDDFQKKWQ 20
                                                                                                                            . .22
label= AI90-111
                                                                                                                                                                                       AI90-111
                                                                                                                                                                                                                                                                        AI93-101
                                                                                                                                                                                                                                                                                                                    AI95-105
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/label= ;
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label= ,
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|abel=
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|abel=
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label=
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-1988;
                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO8904486-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-1999
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Peptide
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Diemer K, Guo N; 1 S, Vandergriff J;

Mi H, Diem Rabkin S,

Campbell MJ, Muruganujan A,

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Lazareva B, Kejariwal

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09-DEC-2003; 2003WO-US038935.
                                                                                                                09-DEC-2002; 2002US-0431879P
                                                                                                                                       (APPL-) APPLERA CORP
                                            WO2004053769-A2.
                                                                                                                                                                         Ladunga I, I
Doremieux O;
                                                                  24-JUN-2004.
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                      Sus scrofa.
                                                                                                                                                             трошав РD,
                                                                                                                                                                                                                                                                     an output
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is baboon apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
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gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                       Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 SALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                          Diemer K, Guo N;
n S, Vandergriff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.8%; Score 108; DB 8; Length 85; 31.9%; Pred. No. 0.0077; tive 20; Mismatches 29; Indels
                               Baboon apolipoprotein A (APO-A) IV precursor protein.
                                                                                                                                                                                                                                            Mi H, Dieme
Rabkin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig apolipoprotein A (APO-A) IV precursor protein.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 47; 113pp; English
                                                                                                                                                                                                                                           Campbell MJ,
Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP87439 standard; protein; 85 AA
                                                                                                                                                                         09-DEC-2003; 2003WO-US038935.
                                                                                                                                                                                                09-DEC-2002; 2002US-0431879P
          09-SEP-2004 (first entry)
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RLLPHANEVSQK 72
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                                                                                                                                                                                                                                                         Lazareva B,
                                                                                                                                                                                                                       (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                        WPI; 2004-480967/45.
                                                                                                                            WO2004053769-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 85 AA;
                                                                                                      Papio anubis.
                                                                                                                                                                                                                                                         Ladunga I,
Doremieux O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-2004
                                                                                                                                                   24 - JUN - 2004
                                                                                                                                                                                                                                            Thomas PD,
                                                                                                                                                                                                                                                                                                                                                   output
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                 baboon,
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biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is pig apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                   Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
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gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 SALGKOLNIKLIDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGIRQEMSKDLEEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                     The invention relates to a browsable database system for use with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.1%; Score 104; DB 8; Length 85; 30.6%; Pred. No. 0.019; ive 20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken apolipoprotein A (APO-A) IV protein.
                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 46; 113pp; English.
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Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RLLPHATEVSOK 72
WPI; 2004-480967/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus.
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A187-105 and smaller peptides contained within this sequence - see FT. Such Apo AI peptides are capable of immunologically minicking a native conserved Apo AI epitope. They may be helpful in the diagnosis of risk of coronary heart disease. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New synthetic peptide from apolipoprotein AIV related protein, useful for raising antibodies, used for diagnosis and treatment of disorders of lipid metabolism.
                                                                                                                                                                                                                                                            New monoclonal antibody and polypeptide antigens - directed against APO AI-HDL epitope, useful in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.8%; Score 97; DB 1; Length 19; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apolipoprotein AIV related protein, AA4RP, peptide.
                                                                                                                                                       (SCRI ) SCRIPPS CLINIC & RES FOUND.
                                                                                                                                                                                                                                                                                                               Claim 2; Table 1-2; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP70773 standard; protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 SKDLEEVKAKVQPYLDDFQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SKDLEEVKAKVQPYLDDFQ 19
                                                                                  88WO-US003903
                                                                                                                    87US-00116248
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12-AUG-2002; 2002FR-00010205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                           Curtiss LK, Smith RR;
                                                                                                                                                                                                                           WPI; 1989-165740/22
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coronary disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 AA;
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                                                                                  02-NOV-1988;
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                                                                                                                    03-NOV-1987;
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              WO8904486-A.
                                               18-MAY-1989
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Matches
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                                                                                                                                                                                                                                                                                                                                           The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is chicken apolipoprotein A (APO-A) IV protein. This sequence is used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 KOLNLKLILDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                    Mi H, Diemer K, Guo N;
Rabkin S, Vandergriff J;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL; coronary artery disease; CAD; Apo AI epitope; AI87-105.
                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 45; 113pp; English.
                                                                                                                    Campbell MJ,
Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apolipoprotein AI (Apo AI) polypeptide
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/label= A193-101
9. .19
/label= A195-105
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|abel= AI90-105
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/label= AI87-101
              09-DEC-2003; 2003WO-US038935.
                                               09-DEC-2002; 2002US-0431879P.
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Bet Local Similarity 30.39,
Thes 21; Conservative
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                                                                                                                    Kejariwal A,
                                                                                                                                        Lazareva B,
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                                                                                  (APPL-) APPLERA CORP
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                                                                                                                                                                                        WPI; 2004-480967/45.
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31-OCT-2002
10-APR-1990
                                                                                                                                                       Doremieux O;
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                                                                                                                Thomas PD,
                                                                                                                                        Ladunga I,
                                                                                                                                                                                                                                                                                output
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                                          Related Protein (AA4RP). The peptide fragment is useful for raising specific antibodies (Ab) against AA4RP, so are useful in immunoassays for detecting or determining AA4RP, especially to identify subjects at risk of developing disorders of lipid metabolism (particularly cardiovascular diseases associated with hyperlipidemia, e.g. coronary disease). Ab are also useful for protein purification and, optionally when conjugated to a toxin or pharmaceutical, for treating the specified diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and
                                                                                                                                                                                                                                                                                           24 DSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLR 83
                                                                                                                                                                                                                                                                                                                 Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein C; APO-C;
                                 present sequence is a peptide fragment of human Apolipoprotein AIV
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mi H, Diemer K, Guo N;
Rabkin S, Vandergriff J;
                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                       16.8%; Score 96.5; DB 6; Length 95; 29.5%; Pred. No. 0.12; tive 21; Mismatches 31; Indels
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Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat apolipoprotein C (APO-C) IV protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP87432 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                             84 QEMSKDLEEVKAKVQPYL 101
                                                                                                                                                                                                                                                                                                                                                                                   ROLQEELEEVKARLOPYM 92
Claim 1; Page 6; 45pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-2003; 2003WO-US038935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-2002; 2002US-0431879P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                         Local Similarity 29.5%
les 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-480967/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004053769-A2.
                                                                                                                                                                                       Sequence 95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ladunga I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP87432;
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in facilitating comparative genomic analysis. The present sequence is rat apolipoprotein C (APO-C) IV protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                         40 KOLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQP
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                             8;
                                                                                                                                              Length 107;
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                                                                                                                                            Query Match 16.5%; Score 95; DB 8;
Best Local Similarity 29.3%; Pred. No. 0.19;
Matches 22; Conservative 18; Mismatches 27
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                                                                                                  Sequence 107 AA;
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December 21, 2004, 12:14:35 ; Search time 144 Seconds (without alignments) 270.861 Million cell updates/sec
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1 DEPPQSPWDRVKDLATVYVD......LEEVKAKVQPYLDDFQKKWQ 109
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1: \( cgn2 \frac{6}\) \text{prodata/2} \text{Pubbaa/USO7} \text{PUBCOMB.pep:*} \)

2: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO6} \text{NEW PUB.pep:*} \)

3: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO6} \text{NEW PUB.pep:*} \)

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7: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO8} \text{NEW PUB.pep:*} \)

7: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO8} \text{NEW PUB.pep:*} \)

8: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO8} \text{PUBCOMB.pep:*} \)

10: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{PUBCOMB.pep:*} \)

11: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{PUBCOMB.pep:*} \)

12: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{PUBCOMB.pep:*} \)

13: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{PUBCOMB.pep:*} \)

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15: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{NEW PUB.pep:*} \)

16: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{NEW PUB.pep:*} \)

17: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{NEW PUB.pep:*} \)

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19: \( cgn2 \frac{6}\) \text{prodata/2} \text{pubpaa/USO9} \text{NEW PUB.pep:*} \)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 109
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Perfect score:
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                                                                                                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	403, App	405, App	276814,	89, Appl	1434, Ap	21, Appl	50, Appl	49, Appl	2, Appli	40, Appl	41, Appl	33, Appl	37, Appl
Description	Sequence	Seguence		Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	US-10-038-854-403	US-10-038-854-405	US-10-424-599-276814	US-10-465-789A-89	US-09-864-408A-1434	US-10-120-508-21	US-10-465-789A-50	US-10-465-789A-49	US-10-487-096-2	US-10-142-238A-40	US-10-142-238A-41	US-10-142-238A-33	US-10-700-340-37
DB	15	15	15	15	11	14	15	12	17	14	14	14	11
% Query Match Length DB	93	93	86	43	64	26	22	22	95	30	30	18	16
% Query Match	57.7	57.7	55.2	39.4	28.1	23.8	20.5	19.4	16.8	16.3	16.3	16.0	15.5
Score	332.5	332.5	318	227	162	137	118	112	96.5	94	94	92	83
Result No.	-	7	Э	4	'n	9	7	œ	6	10	11	12	13

APPLICANT: Acklud, Kameda, Ackluda, Ackluda, Ackluda, Ackluda, Meera APPLICANT: Gusev, Vladimir Y APPLICANT: Gangolli, Esha A APPLICANT: Gangolli, Esha A APPLICANT: Gangolli, Esha A APPLICANT: Shenoy, Siaojia S APPLICANT: Restelli, Luca APPLICANT: Casman, Stacie J APPLICANT: Boldog, Ferenc APPLICANT: Burgess, Catherine E APPLICANT: Burgess, Catherine E APPLICANT: Gunther, Erik APPLICANT: Shithson, Glennda APPLICANT: MacDougall, John R APPLICANT: MacDougall, John R APPLICANT: MacDougall, John R TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding CURRENT APPLICANTON UNBER: US/10/038,854

14 89 15.5 30 14 US-10-142-23 16 87 15.1 18 17 15 US-10-142-23 18 87 15.1 18 14 US-10-142-23 19 86 14.9 30 14 US-10-142-23 20 86 14.9 30 14 US-10-142-23 21 88 14.8 30 14 US-10-142-23 22 88 14.8 30 14 US-10-142-23 23 84 14.6 18 14 US-10-142-23 24 84 14.6 18 14 US-10-142-23 25 83 14.4 18 14 US-10-142-23 26 87 11.7 72 16 US-10-142-23 27 74 12.8 14 18 14 US-10-142-23 28 67.5 11.7 72 16 US-10-142-34 31 65 11.5 12.8 14 US-10-142-34 32 66 11.5 13 15 US-10-674-76 33 65 11.5 13 15 US-10-674-76 34 65.5 11.9 10 14 US-10-142-59 44 65.5 10.9 97 17 US-10-674-75 45 61 10.0 10 10 15 US-10-674-75 45 61 10.0 10 10 15 US-10-674-75 46 61.5 10.7 99 15 US-10-674-75 47 61.5 10.7 99 15 US-10-674-75 48 61.5 10.7 99 15 US-10-674-75 48 61.5 10.7 99 15 US-10-674-75 48 FESULT I APPLICANT: SPYTEK, Kimberly A APPLICANT: Worlet, Corine APPLICANT: Walpan, Andrew J APPLICANT: Walpankar, Uriel M APPLICANT: Walpankar, Uriel M APPLICANT: Shinkete, Richard A APPLICANT: Shinkete, Uriel M APPLICANT: Tenhermar, Uriel M APPLICANT: Spaderna, Steven K APPLICANT: Spaderna, Steven K APPLICANT: Reknida Ramen
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14 89 15 16 89 16 17 17 17 18 89 18 87 19 86 20 86 20 86 22 88 22 88 22 88 23 66 23 30 67 24 88 33 66 33 66 33 66 34 65.5 42 65.5 44 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 61.5 45 6
RESULT APPPLT AP

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APPLICANT: LA ROSA Thomas J
APPLICANT: LA ROSA Thomas J
APPLICANT: LA ROSA Thua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                            THIS REFERENCE: 21402-22
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR PELICATION NUMBER: 60/258,928
PRIOR PELICATION NUMBER: 60/258,415
PRIOR PELING DATE: 2010-10-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR PELING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-03-03
PRIOR PILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-18
PRIOR PELING DATE: 2001-04-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.7%; Score 332.5; DB 15; Length 93; Best Local Similarity 71.9%; Pred. No. 4e-25; Matches 69; Conservative 0; Mismatches 0; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Mucleic Acids Encoding Same
FILE REFERENCE: 21402-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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US-10-424-599-276814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 109
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Pred. No. 9.8e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 276814, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.4%;
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-038-854-405
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                               PRIOR PELICATION NUMBER: 60/259, 415
PRIOR APPLICATION NUMBER: 60/259, 415
PRIOR APPLICATION NUMBER: 60/259, 415
PRIOR PILING DATE: 2000-10-09
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279, 833
PRIOR PILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PILING DATE: 2001-04-13
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57.7%; Score 332.5; DB 15; Length 93;
Best Local Similarity 71.9%; Pred. No. 4e-25;
Matches 69; Conservative 0; Mismatches 0; Indels 27
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Publication No. US20040022781A1
GENERAL INFORMATION:
          60/258,928
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APPLICANT: Spytek, Kimberly A
APPLICANT: Nolenc, Adam R
APPLICANT: Wornet, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiachong
APPLICANT: Liu, Xiachong
APPLICANT: Shankets, Nichard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
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Edinger, Shlomit R
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Gusev, Vladimir Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smithson, Glennda
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gusev, Vladimir )
Gangolli, Esha A
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Gunther, Erik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-038-854-403
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                                                                                                                                                   Sequence 21, Application US/10120508
Publication No. US20030191057A1
GENERAL INFORMATION:
APPLICANT: FOCELANAN ALAN
APPLICANT: NAVAB, MOHAMAD
FITTLE OF INVENTION: G-TYPE PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 407T-301100US
CURRENT APPLICATION UNMBER: US/10/120,508
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 32
SOFTWARR: PATENTIN VEFFION 3.0
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                          25 DEPQSQWDRVKDFATVYVDAVKDSGRNYVSQFESSTLGQQ 64
2 EPPOSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.8%; Score 137; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-06; Matches 26; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 9.8e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/10465789A

Publication No. US2004005384A1

GENERAL INFORMATION:

APPLICANT: Sligar, Stephen G

APPLICANT: Bayburt, Timothy H

APPLICANT: Schuler, Mary A

APPLICANT: Schuler, Mary A

APPLICANT: Civjan, Natanya R

APPLICANT: Ilia G. Denisov

TITLE OF INVENTION: Membrane Scaffold Proteins

FILE REFERENCE: 87-00A

CURRENT APPLICATION NUMBER: US/10/465,789A

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: 60/252,233

PRIOR APPLICATION NUMBER: 60/252,233

PRIOR APPLICATION NUMBER: 2000-11-20

NUMBER: DEFO. TIN MAC. 00.011-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%; Pred. No. 9.8
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic D peptide. US-10-120-508-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 WDRVKDLATVYVDVLKDSGRDYVSQF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WDRVKDLATVYVDVLKDSGRDYVSQF 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 89
SOFWARE: Patentin version 3.1
SEQ ID NO 50
LENGTH: 22
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ORGANISM: Artificial Sequence
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                                                                                                             RESULT 6
US-10-120-508-21
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Enco TITLE OF INVENTION: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1334
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                                                    25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVDSTFSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DEPPOSPWDRVKDLATVYVDVLKDSGRDYVSQPEGSALGKQLN 43
                                                                                                                                                                                                                                                                                                                               APPLICANT: Sligar, Stephen G
APPLICANT: Blayburt, Timothy H
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Marany A
APPLICANT: Schuler, Marany A
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Tila G. Denisov
TITLE REFERENCE: 87-00A
CURRENT PRILING DATE: 2003-6-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR PILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1434, Application US/09864408A Publication No. US20040009474A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                US-10-465-789A-89
; Sequence 89, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: sequence of GLOB
US-10-465-789A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                             RE 62
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US-09-864-408A-1434
                                                                                                                                                      85 RE 86
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US-10-142-238A-41

US-10-142-238A-41

Sequence 41, Application US/10142238A

Publication No. US20030087819A1

GENERAL INFORMATION:

APPLICANT: BIGLICK; JOHN K.

TITLE OF INVENTY DATE: CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES

FILE REFERENCE: 1B-1705

CURRENT APPLICATION NUMBER: US/10/142,238A

CURRENT PELING DATE: 2002-08-19

PRIOR PELING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 84

SOFTWARE: Patentin version 3.1

SEQ ID NO 41

LENGTH: 30

TAPE: DATE: CONTAINED TO SET T
Sequence 40, Application US/10142238A
Publication No. US2003008781941
GENERAL INFORMATION:
APPLICANT: Bielicki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REFERENCE: 1B-1705
CURRENT PFLIANG DATE: 2002-08-19
PRIOR PPLIANG DATE: 2002-08-19
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LEAGTH: 30
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Publication No. US2030087819A1

GENERAL INFORMATION:
APPLICANT: Bielicki, John K.
11TLE OF INTENTION: CYSTBINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
11TLE REPERBUCE: 1B-1705

CURRENT APPLICATION NUMBER: US/10/142,238A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.3%; Score 94; DB 14; Length 30; 95.0%; Pred. No. 0.034; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(30)
COTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-40
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COATION: (1). (30)
COTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LPLKLLDNWDSVTSTFSKLR 30
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ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.04
Matches 19; Conservative
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US-10-142-238A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 DSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
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Publication No. US20040197823A1
GENERAL INFORMATION:
APPLICANT: GRANT SA
TITLE OF INVENTION: Compositions and Methods for the assay of AA4RP
FILE REFERENCE: B0157W0
CURRENT APPLICATION NUMBER: US/10/487,096
CURRENT FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 95
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                                                                                                                                                               | FUBLICATION NO. USZU040053384A1 |
| GENERAL INFORMATION: |
| APPLICANT: S193T, Stephen G |
| APPLICANT: S193T, Timothy H |
| APPLICANT: Schuler, Mary A |
| APPLICANT: Civyan, Natanya R |
| APPLICANT: Civyan, Natanya R |
| APPLICANT: Yelena V Grinkova |
| FILE REFERENCE: 87-00A |
| CURRENT APPLICATION NUMBER: US/990,087 |
| PRIOR PLILING DATE: 2001-11-20 |
| PRIOR PLILING DATE: 2001-11-20 |
| NUMBER OF SEQ ID NOS: 89 |
| SEQ ID NO 49 |
| LENGTH: 22 |
| LENGTH: 23 |
| LENGTH: 24 |
| LENGTH: 24 |
| LENGTH: 24 |
| LENGTH: 25 |
| LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: artificial sequence of Helix 1
US-10-465-789A-49
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19.4%; Score 112; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 22; Conservative 0; Mismatches 0;
                                                           US-10-465-789A-49; Sequence 49, Application US/10465789A; Publication No. US20040053384A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 LKLLDNWDSVTSTFSKLREQLG 65
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75 RQLQEELEEVKARLQPYM 92
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Best Local Similarity
Matches 23; Conserva
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US-10-142-238A-40
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RESULT 15
US-10-142-238A-43
is Sequence 43, Application US/10142238A
is Sequence 43, Application US/10142238A
is Datation No. US20030087819A1
is GENERAL INFORMATION:
is APPLICANT: Bielicki, John K.
is APPLICANT: Bielicki, John K.
is TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
is CURRENT APPLICATION NUMBER: US/10/142,238A
is CURRENT PILING DATE: 2002-08-19
is PRIOR APPLICATION NUMBER: US 60/289,944
is RIOR FILING DATE: 2001-05-09
is NUMBER OF SEQ ID NOS: 84
is SOFTWARE: PatentIn version 3.1
is SEQ ID NO 43
is LENGTH: 30
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Pred. No. 0.1;
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Pred. No. 0.1;
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90.0%; Pred. No. v...
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; OTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-39
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CCATION: (1)..(30)
COTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-43
                            PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SEQ ID NO 39
LENGTH: 30
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         2002-08-19
                                                                                                                                                                                                                     TYPE: PRT ORGANISM: ARTIFICIAL SEQUENCE
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ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 90.00
- Then 18; Conservative
         CURRENT FILING DATE:
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Fublication No. US20040203023A1
GENERAL INFORMATION:
FAPLICAAT: Herath, Herath Mudiyanselage Athula Chandrasiri
TITLE OF INVENTION: CANCER
FILE OF INVENTION: CANCER
FILE OF INVENTION: CANCER
FILE REFERENCE: 2543-1-032
CURRENT APPLICATION NUMBER: US/10/700,340
CURRENT PELING DATE: 2003-11-03
FRIOR FILING DATE: 2002-05-02
FRIOR FILING DATE: 2001-05-02
FRIOR PELING DATE: 2001-06-14
FRIOR PELING DATE: 2001-08-14
FRIOR PELING DATE: 2001-08-14
FRIOR PELING DATE: 2001-08-14
FRIOR PELING DATE: 2001-08-16
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US-10-142-238A-39
; Sequence 39, Application US/10142238A
; Sequence 39, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
; APPLICANT: Bielicki, John K.
; TITLE OF INVENITON: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
; FILE REFERENCE: IB-1705
; CURRENT APPLICATION NUMBER: US/10/142,238A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 18; 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 16; 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.0%; Score 92; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%; Score 89; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE

LOCATION: (1)..(18)

COTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-33
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SSOFTWARE: Patentin version 3.1
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKLLDNWDSVTSTFSKLR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LKLLDNWDSVTSTFSKLR 61
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EQLGPVTOEFWDNLEK 16
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Best Local Similarity 100.0
Matches 16; Conservative
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2004, 12:22:02; Search time 38 Seconds

(without alignments)

275.990 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_133

Sequence: 1 DEPPQSPWDRVKDLATVYVD......LEEVKAKVQPYLDDFQKKWQ 109

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 44103
```

Minimum DB seq length: 0
Maximum DB seq length: 109
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: Dirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

antifreeze protein hypothetical prote hypothetical prote hypothetical prote apolipoprotein AI apolipoprotein A-I apolipoprotein A-I hypothetical prote ski-related protei neurofilament-M ho hypothetical prote hypothetical prote hypothetical cytos hypothetical 10.0 transposase BMEII0 transposase BMEII0 hypothetical prote homeotic protein E hypothetical prote conserved hypothet nonhistone chromos prote probable molybdopt MHC HLA-DR7 DQ-bet prote virulence-associat apolipoprotein A-I integral membrane HLA DR-beta-I hypothetical hypothetical hypothetical Description SUMMARIES A05313 G86722 B46598 A60094 F71511 D95153 D82445 JU0038 AI3537 A72222 B69466 E34510 H81298 I55994 H69767 I72481 AB3643 168742 C90225 C90342 A59010 **D97844** F81669 C65120 AF3532 Query Match Length DB 100.5 100.2 100.2 100.2 100.2 100.2 100.2 11.5 10.9 10.9 10.7 10.6 10.6 Score 60.5 59.5 59.5 59 58.5 58.5 58.5 58.5 57.5 57.5 57.5 57.5 63 63 63 61.5 Result No. 

hypothetical prote	hypothetical prote	apolipoprotein C-I	M protein precurso	4-oxalocrotonate t	M-like protein enn	M-like protein enn	M-like protein enn	uncharacterized sm	M-like protein enn	hypothetical prote	hypothetical prote	conserved domain p	transforming prote	homeotic protein E	hypothetical prote
B95955	AH2558	LPHUC1	S60832	C89912	S62075	S61821	S61805	H96904	S62082	T17961	G98009	A95142	A46598	F34510	875479
7	N	н	7	~	(1)	N	~	7	7	7	~	~	7	~	7
83	108	83	82	62	83	88	94	97	105	83	100	100	101	109	61
6.6	6.6	9.8	7.6	9.6	9.6	9.6	9.6	9.6	9.6	9.5	9.5	9.5	9.5	9.5	9.5
57	57	56.5	99	55.5	55.5	55.5	55.5	55.5	55.5	55	55	22	22	52	54.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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apolipoprotein AI - goose (fragment)

CjSpecies: Anser anser (domestic goose)

CjSpecies: Anser anser (domestic goose)

CjSpecies: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

CjAccession: 867972

RiHermier, D.; Sellier, N.; Rousselot-Pailley, D.; Forgez, P.

Bur. J. Blochem. 234, 586-591, 1995

A;Title: Characterization of apolipoproteins B-100, AI and C from plasma lipoprotein in A;Reference number: 867972; MUID:96128192; PMID:8536707

A;Accession: 867972

A;Molecule type: protein

A;Molecule type: protein

A;Residues: 1-34 CHER.

A;Residues: 1-34 CHER.

A;Cross-references: UNIPROT:Q9PRR6

C;Superfamily: apolipoprotein A-I
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C;Species: Coturnix coturnix japonica (Japanese quail)
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 18-Mug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A5686
B;Ocku, H.; Ishikawa, M.; Nagata, J.; Toda, T.; Chinen, I.
B;Ochim. B;Ophys. Acta 1167, 22-28, 1993
A;Title: Lippprotein and apoprotein profile of Japanese quail.
A;Reference number: A56866; MUID:93213845; PMID:8461329
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A;Note: sequence extracted from NCBI backbone (NCBIP:128831)
A;Note: this protein was found primarily as a 26K apoprotein C;Superfamily: apolipoprotein A-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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50.0%; Pred. No. 0.0099;
iive 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 2;
Pred. No. 0.0093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE
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54.5%;
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Best Local Similarity 50.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-36 <OKU>
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RESULT 1
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Gaps

12;

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C;Accession: A60094
R;Sharpe, C.R.
Development 103, 269-277, 1988
A;Title: Developments expression of a neurofilament-M and two vimentin-like genes in Xe A;Reference number: A60094; MUID:89136789; PMID:3224553
                                                                                                                                                                                                                                                                                                                                                                                                                                   41 QLNLKLLIDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 SGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVT------QEFWDN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurofilament-M homolog XIF6 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
A;Molecule type: mRNA
A;Residues: 1-56;57-99 <NAG>
A;Cross-references: UNIPOT:Q9PSS3
A;Note: sequence extracted from NCBI backbone (NCBIP:134568, NCBIP:134572)
C;Superfamily: ski transforming protein
C;Keywords: DNA binding; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 10.9%; Score 63; DB 2; Length 104; Il Similarity 25.6%; Pred. No. 1.3e+02; 20; Conservative 15; Mismatches 27; Indels
                                                                                                                                                                                                                                                                    Query Match
10.9%; Score 63; DB 2; Length 99;
Best Local Similarity 32.3%; Pred. No. 1.3e+02;
Matches 20; Conservative 15; Mismatches 15; Indels
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Residues: 1-104 CSHA>
A;Crosa-references: UNIPROT:013099; UNIPROT:013098
C;Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 LEKETEGLRQEMSKDLEE 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                  MyAlternate names: apo-A-I
CiSpecies: Erythrocebus patas (red guenon, hussar)
CiSpecies: Erythrocebus patas (red guenon, hussar)
CiSpecies: Erythrocebus patas (red guenon, hussar)
CiDate: 05-Uun-1987 #sequence_revision 05-Uun-1987 #text_change 09-Jul-2004
CiAccession: A05313 #sequence_revision 05-Uun-1987 #text_change 09-Jul-2004
CiAccession: A05313 #sequence_revision 05-Uun-1987 #text_change 09-Jul-2004
Airtle: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus Airtle: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus Airtle: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus Airtle: Characterization of the Plasma lipoprotein Airtle: Characterization of the Distance University and Airtle: Characterization of the Brythrocebus Airtle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyaccession: G86722
RyBolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Ress. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Racession: G86722
A; Status: presiminary
A; Molecule type: DNA
A; Residues: 1-79 <STO>
A; Cross-references: UNIPROT:09CHE9; GB:AE005176; PID:g12723703; PIDN:AAK04881.1; GSPDB:G G; Genetics:
A; Gene: yhja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein yhja [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
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C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Nagase, T.; Nomura, N.; Ishii, S.
J. Biol. Chem. 268, 13710-13716, 1993
A;Ritle: Complex formation between proteins encoded by the ski gene family.
A;Reference number: A46598, MUID:93293901; PMID:8514802
A;Accession: B46598
A;Status: preliminary; not compared with conceptual translation
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85.0%; Pred. No. 0.013;
tive 2; Mismatches 1.
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Best Local Similarity 31.3*
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.0 Matches 17; Conservative
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EDVAEKF 66
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Gaps

16;

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virial vaporiated protein vapa homolog H11251 - Haemophilus influenzae (strain Rd KW2 C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision W.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A; Fileischmann, R.D.; Achthors, Godayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Hille: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q57089; GB:U32805; GB:L42023; NID:g1574180; PIDN:AAC22901.1,
C;Superfamily: virulence-associated protein vapA
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: H64112
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <TIGR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB 1;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.9%;
23.9%;
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Best Local Similarity
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hypothetical protein SSO8938 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90342
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q97XE7; GB: AE006641; NID: 913815050; PIDN: AAK41994.1; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F71511
hypothetical protein CT466 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species Chlamydia trachomatis
C;Species Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: F71511
C;Accession: F71511
S;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach, R;Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- 51
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antifreeze protein LS-12 - longhorn sculpin
C;Species: Myoxocephalus octodecimspinosis (longhorn sculpin)
C;Species: Myoxocephalus octodecimspinosis (longhorn sculpin)
C;Date: 10-Oct-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C;Accession: A59010
R;Deng, G:;Andrews, D.W.; Laursen, R.A.
R;Deng, G:;Andrews, D.W.; Laursen, R.A.
A;Reference number: A59010
A;Reference number: A59010
A;Status: preliminaria
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.6%; Score 61; DB 2; Length 75; 22.8%; Pred. No. 1.3e+02;
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        --QELKKRVEELEKKVK 75
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A; Experimental source: blood plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 23; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: C90342
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-75 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SSO8938
            61
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C;Genetics:
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90225
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Chao, N.J.; Timmerman, L.; McDevitt, H.O.; Jacob, C.O.
Immunogenetics 29, 231-234, 1989
A;Title: molecular characterization of mhc class ii antigens (beta-1 domains) in the A;Reference number: 154455; MUID:89197303; PMID:2784784
A;Accession: 168742
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                     10 RVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQ 69
                                                                                                                                                               ----TP 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integral membrane protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: RT1.B
C,Superfamily: class II histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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            18;
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        31; Indels
                                                                                                                              24 KISDLAQI-LDVHRNTASNIVN--NSSRITLEMAVKLAKVPDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 SKIREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-96 <RES>
                                                                                                                                                                                                                                        70 EFWDNLEKETEGLRQEMSKDLEEVKAKVQPYL 101
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        21;
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60 YWN--KQYLEQTRAELDR 75
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Best Local Similarity 21.8*
Matches 22; Conservative
        Conservative
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A;Molecule type: DNA
A;Residues: 1-75 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: I68742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: C90225
22;
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        Matches
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Search completed: December 21, 2004, 12:34:46
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type:
A;Molecule type:
A;Genetical source: serotype D, strain UW-3/Cx
C;Genetical:
A;Genetical type:
C;Superfamily: conserved hypothetical protein CP0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-107 -KUR>
A;Cross-references: UNIPROT:Q97QA2; GB:AE005672; PIDN:AAK75421.1; PID:g14972804; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Circuston 195153

RiTettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, C.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, C.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hockey, E.K.; Holt. I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Alther Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Accession: D95153
A;Accession: D95153
A;Althory DAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CiAccession: D82445
RiHeidelberg, J.F.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
Alticle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein VCA0551 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SP1323 [imported] - Streptococcus pneumoniae (strain TIGR4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 SPWDRVKDLATVYVDVLKDSGRDY-----VSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60
                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Streptococcus pneumoniae
C;Date: 03-Aug_2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                 Length 109;
                                                                                                                                                                                                                                                                                                                   28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 60.5; DB 2; 23.5%; Pred. No. 2.2e+02; tive 17; Mismatches 35;
                                                                                                                                                                                                                                                            10.6%; Score 61; DB 2; I 25.3%; Pred. No. 2.1e+02; iive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 LEEVKAKVQPYLDDFQKKW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [||::::| |:::| :
LEEIRSVIQRILETDKKNY 93
                                                                                                                                                                                                                                                                                      Local Similarity 25.3% nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.5%
Matches 23; Conservative
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: SP1323
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Matches
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A;Cross-references: UNIPROT:Q9KM38; GB:AE004386; GB:AE003853; NID:g9657957; PIDN:AAF964! A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VCA0551 A;Gene: VCA0551 A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JU0038
Hayashi, T.; Hayashi, H.; Iwai, K.
J. Biochem. 105, 577-581, 1989
A;Title: Tetrahymena HMG nonhistone chromosomal protein. Isolation and amino acid sequen
A;Reference number: JU0038; MUID:89340384; PMID:2760016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Genetic code: SGC5
A,Genetic code: SGC5
C,Keywords: chromosomal protein, DNA binding; nucleus; phosphoprotein
C,Keywords: chromosomal protein, DNA binding; nucleus; phosphoprotein
F, 8-83/Domain: Hyd Dox homology (HMG1)
F,16,43/Binding site: phosphate (Seri (covalent) (partial) #status experimental
F,42/Binding site: phosphate (Thr) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nonhistone chromosomal protein HMG - Tetrahymena pyriformis
C;Species: Tetrahymena pyriformis
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 PPKRP-----LSAFF--LFKQHNYDQVKKENPNAKITELTSMIAEKWKHVT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 QEFWDNLEKETEGLRQE------MSKDLEEVKAKVQPYLDD 103
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A;Molecule type: protein
A;Residues: 1-99 <HAY>
A;Cross-references: UNIPROT:P40625
A;Note: this HMG iss similar to the central part of vertebrate HM
A;Note: Ser-16 and Thr-42 and/or Ser-43 are 6-7% phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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158, App 26113, A 8, Appli 8, Appli 41, Appl 17, Appl

Sequence Sequence Sequence Sequence

Sequence 1 Sequence 4 Sequence 6

Sequence 3 Sequence 3 Sequence 3

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

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GENERAL INFORMATION:

APPLICANT: Cuttiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: The Scrippe Research Institute, Office of ADDRESSE: Patent Counsel
ADDRESSE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: P. 1923.7
COMPUTER READABLE FORM:
MEDIUM TYPE: P. 1929y disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIPICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRILING DATE: 06-JUN-1991
PRILING DATE: 06-JUN-1991
PRILING DATE: 07-JUN-1991
PRILING DATE: 07-JUN-1991
PRILING DATE: 07-JUN-1991
ATTORNEY/AGENT INPORMATION:
NAME: FILLING, THOMBER: PCT/US 91/04038
PTILING DATE: 07-JUN-1991
ATTORNEY/AGENT INPORMATION:
NAME: FILLING, THOMBER: MANDER: 
US-09-874-923-61

US-08-710-749-12

US-09-17-875A-13

US-08-710-749-28

US-09-147-875A-28

US-09-147-875A-28

US-08-867-087B-3

US-09-614-912-158

US-09-614-912-158

US-09-48-756A-26113

US-09-182-175A-8

PCT-US92-06412-8

US-08-025-038-41

US-08-710-749-17

US-09-134-000C-615

US-09-114-09-17

US-09-114-09-11
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TELECOMMUNICATION INFORMATION:
TELEPHAN: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08292870 ; Patent No. 5814467
    CITY: La Jolla
STATE: California
COUNTRY: US
    STREET:
CITY: La
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US-08-292-870-2
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Sequence 5725, A
Sequence 34, Appli
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-292-870-1

US-08-292-870-4

US-08-292-870-3

US-08-392-946-5

US-08-333-277-5

US-08-333-277-5

US-08-313-599C-6681

US-08-21-853-11

US-08-21-853-11

US-08-147-875-16

US-09-147-875-16

US-09-147-97-17

US-08-170-743-10

US-08-170-743-10

US-08-170-743-10

US-08-170-743-10

US-08-170-749-10

US-08-170-749-10
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US-09-565-501A-61
US-09-639-206A-61
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Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 109
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No.
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APPLICANT: Curities, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Bannet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.8%; Score 114; DB 2; Length 25; Best Local Similarity 95.7%; Pred. No. 3.5e-05; Matches 22; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPL
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RR: TSRI 210.1 D1
                                         1 EMSKDLEEVKAKVQPYLDDFQKKWQ 25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  RESULT 3
10S-08-292-870-4
Sequence 4, Application US/08292870
Patent No. 5814467
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; Patent No. 5814467
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-292-870-3
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Sequence 1, Application US/08292870

Patent No. 58144671

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Banka, Carole L

APPLICANT: Manna Systems FOR QUANTIFYING APO AI, AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 4

CORRESPONDENCES: 4

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STRET: La Jolla

CTTY: La Jolla

STATE: California

COUNTRY: US

TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS

TITLE OF INVENTION: METHODS

TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS

TITLE OF INVENTION: APO AI POLYPEPTION OF TITLE APO 
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ZIP: 92037
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: OF-JUN-1991
PRIOR APPLICATION NUMBER: US 07/711,333
FILING DATE: OF-JUN-1991
PRIOR APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: OF-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REFERENCE/DOCKET 107-401-191
TELEPHONE: 619-54-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LINFORMATION CALIGA
TELEFAX: A A A AMICO ACIGS
TELEMETAL
                                                                                                                                                                                                                                                                                                                                                                                               83 RQEMSKDLEEVKAKVQPYLDDFQKKWQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RQEMSKDLEEVKAKVQPYLDDFQKKWQ 27
                                         MOLECULE TYPE: peptide;
FRAGMENT TYPE: internal
US-08-292-870-2
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linear
    TOPOLOGY:
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US-08-292-870-1
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Gaps

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Sequence 5, Application US/0833577

Patent No. 5786206

GENERAL INFORMATION:
APPLICANT: Smith, Raju
APPLICANT: Smith, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Young, Stephen G.
APPLICANT: Curties, Linda K.
TITLE OF INVENTION: Lipportotein Assays Using Antibodies to a
TITLE OF INVENTION: Lipportotein Assays Using Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milmanow, Ltd.
ADDRESSEE: Milmanow, Ltd.
                            APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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14.1%; Score 81; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          CAPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC Compatible
COMPUTER: EMB PC Compatible
CORERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/959,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELEPHONE: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LELEPAK: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LEMGTH: 16 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 180 No. 5786206th Stetson, Suite 4700 CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Joseph L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 KVQPYLDDFQKKWQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVOPYLDDFOKKWO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-07-959-946-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-333-577-5
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                            APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Banka, Carole L
APPLICANT: Bornet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8 CITY: La Jolla STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 83; DB 2; Length 32; 93.8%; Pred. No. 0.071; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Xaa can be either E (Glu) or F (Phe)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRATING SYSTEM: PC-DoS/MS-DoS
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION 07-31
PRIOR APPLICATION NUMBER: US 07/534,761
PRIOR APPLICATION NUMBER: US 07/11,333
PRIOR APPLICATION NUMBER: US 07/711,333
FILING DATE: 07-JUN-1991
PRIOR APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
PRIOR APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
APPLICATION NUMBER: 34,163
REGISTRATION NUMBER: 32,123
INFORMATION FOR SEQ 1D NO: 3:
ELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 KAKVQPYLDDFQKKWQ 109
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Matches 15; Conservative
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FRAGMENT TYPE: internal
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 92037
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US-07-959-946-5
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Gaps

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TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Smith, Raju
APPLICANT: Smith, Raju
APPLICANT: Witztum, Joseph L.
TITLE OF INVENTION: Lipporterin Assays Using Antibodies to a TITLE OF INVENTION: Lipporterin Assays Using Antibodies to a TITLE OF INVENTION: Lipporterin Assays Using Antibodies to a TITLE OF INVENTION: Lipporterin Assays Using Antigens UNDERSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Lid.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
CITY: Chicago
CITY: Chicago
CITY: Chicago
CITY: Chicago
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: BEATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 1920109
CLASSIFICATION NUMBER: US 07/901,706
FILING DATE: 18-104-1992
ATTORNEY/AGENT INFORMATION:
TELEPAN: GARATERISTICS:
LENGTH: 16 amino acids
TELEFAX: G12186-5400
INFORMATION FOR SEQ ID NO: 5:
BEQUERE CHARACTERISTICS:
LENGTH: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIPICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.,
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 26,780
TELECOMMUNICATION INFORMATION:
TELEPAX: (312)616-5400
INFORMATION ESQ.ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: APPLICATION INFORMATION:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 KVQPYLDDFQKKWQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-333-577-5
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US-08-685-764-4

Sequence 4, Application US/08685764

Sequence 4, Application US/08685764

Sequence 4, Application US/08685764

GENERAL INFORMATION:

APPLICANT: MAKI, NOBENU

APPLICANT: YAGI, SHINTARO

ITILE OF INVENTION: ANTIGENIC PEPTIDES FOR GROUPING

ITILE OF INVENTION: HEPATITIS C VIRUS, KIT COMPRISING THE SAME AND

ITILE OF INVENTION: METHODS FOR ITS GROUPING USING THE SAME

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

ADDRESSEE: OFFICENCE ADDRESS:
                                                                                                                                 Gaps
                                                                                                                                 ö
                                                                               Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,764
                                                                            Score 81; DB 5;
Pred. No. 0.048;
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/092,192
FILING DATE: 15-ULL-1993
APPLICATION NUMBER: UP 212061/92
FILING DATE: 16-ULL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 316634/92
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 316535/92
FILING DATE: 30-CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 104754/93
FILING DATE: 30-APR-193
ATTORNEY/AGNT INFORMATION:
REGISTATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 42822
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 523-3400
TELEFAX: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: 1002 STRE UR
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          Query Match
14.1%; Soc
Best Local Similarity 100.0%; Pi
Matches 14; Conservative 0;
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CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                                                 96 KVQPYLDDFQKKWQ 109
                                                                                                                                                                                                                                 1 KVOPYLDDFOKKWO 14
, MOLECULE TYPE: protein PCT-US92-08634-5
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MOLECULE TYPE: peptide
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FILING DATE: 12-MAY-1994
                                                                                                                                                                                                   LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LECURES 201 TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                        peptide
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: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
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US-08-850-917-11
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COUNTRY:
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                                                                                        39 GKQLNLKLLD-NWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG---LRQEMSKDLEEVK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 67.5; DB 1; Length 87; 24.2%; Pred. No. 9.7; tive 22; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%; Score 67; DB 4; Length 105; 28.4%; Pred. No. 14; tive 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08241853
Patent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanatusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
                                                                                                                                    73 DNLEKETEGLRQEMSKDLEEVKAKVQ---PYLDDF 104
                                                                                                                                                           Sequence 6681, Application US/09513999C Batent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 28.4% hes 19; Conservative
                 Best Local Similarity 24.29
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6681
LENGTH: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackeneack
STATE: New Jersey
COINTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 AKVOPYL 101
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ZIP: 07601
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   Query Match
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Matches
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-----SGRDYVSQFEGS--ALGK 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 66.5; DB 1; Length 105; 27.7%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: US-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION PATA:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 K-HKDFLEELEESRGVMEKLEQQAQGFPEEFRDS 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600-1-078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                  REPERENCE DOCKET NUMBER: 600-
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISICS:
LENGTH: 105 amino acids
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsg., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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20 PFEKLADLAREDLEAHALKGTKYIEDLKG-AVKKDLGYELLKPYDGTRELIKKIKDEDPG 78
                                                                                                                                                                                                                                                                                Sequence 57235, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICAMT: Homburger et al.
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094

CURRENT PILING DATE: 1999-03-17

CURRENT FILE NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 57235
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                                                                                               Gaps
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                                                   Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.9%; Score 63; DB 4; Length 103; Best Local Similarity 28.6%; Pred. No. 34; Matches 18; Conservative 13; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.9%; Score 63; DB 4; Length 106; Best Local Similarity 23.9%; Pred. No. 36; Matches 21; Conservative 24; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4439 Application US/09621976
Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2.
CURRENT APPLICATION UNMER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER: OF SEQ ID NOS: 19335
                                                   DB 3;
                                                11.0%; Score 63.5; E
51.9%; Pred. No. 12;
:ive 4; Mismatches
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                                                                                                                                                                  59 KLREQLGPVTQEFWDNLEKETEGLRQE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster US-09-270-767-57235
                                                                                               14; Conservative
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US-09-621-976-4439
                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patent.pm
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US-09-270-767-57235
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US-09-621-976-4439
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LENGTH: 106
      US-09-695-458-9
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ORGANISM: 1
                                                   Query Match
                                                                                             Matches
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Patent No. 6380361
GENERAL INFORMATION:
APPLICANT: CONKIN., Darrell C.
APPLICANT: Taft, David W.
TITLE OF INVENTION: Educational Kit and Method Containing No. 6380361el Alpha Helical
TITLE OF INVENTION: Beducational Kit and Method Containing No. 6380361el Alpha Helical
TITLE OF INVENTION: Brotein-34
CURRENT APPLICATION NUMBER: US/09/695,458
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/162,623
PRIOR APPLICATION NUMBER: 60/162,623
PRIOR APPLICATION NUMBER: 60/162,623
RUMBER OF SEQ ID NOS: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09147875A
Patent No. 6638516
GENERAL INFORMATION:
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REFERENCE: 454312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                          DB 2; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 11.4%; Score 65.5; DB 4; Length 99; Local Similarity 24.2%; Pred. No. 18; Onservative 19; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDD 103
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                                                                                                                                                                                                                                                                                                                                                                                                                       71 K-HKDFLEELEESRGVMEKLEQQAQGFPEERDS 103
                                                                                                                                                                                                                                                                                                                                                                                      41 OLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDN 74
                                                                                                                                                                                                        11.5%; Score 66.5; D
27.7%; Pred. No. 15;
tive 11; Mismatches
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                                                                                                                                                                                                                                                                                                8 WDRVKDLATVYVDVLKD----
LENGTH: 105 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                             Best Local Similarity 27.74
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-147-875A-16
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LENGTH: 50
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Search completed: December 21, 2004, 12:33:58 Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 21, 2004, 12:05:04; Search time 38 Seconds (without alignments) 98.749 Million cell updates/sec Run on:

US-09-803-918A-2_COPY_75_113 201 1 DSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKD 39 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

9448 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 41

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Descr	!	H81592 hypothetical	G84147 hypothetical	AH1838 cytochrome c6	E60977 14-3-3 protei	S74192	T07516	hypothetical	2	myohemerythi			P82012 hypothetical prote	$\mathbf{H}$		hypothetical	B56635 tubulin alpha chai		A59005 thymosin beta - se	S17432 H+-transporting tw	91	SECH secretin - chicken		H72312 hypothetical prote		fructosyllysi		
	DB	1		7			7		7	~	~	~	~	7	~	N	~	~	~	7	7	7	7	7	~	7	~	~	
	Length	33	40	34	35	19	30	40	39	27	31	34	35	35	39	40	31	33	37	40	29	15	27	29	30	35	35	36	•
	Query	9.9	8.4	7.9	7.9	6.9	6.9	6.9	6.4	6.2	5.9	5.9	5.9	5.9	5.9	5.9	5.4	5.4	5.4	5.4	5.2	4.9	4.9	4.9	4.9	4.9	4.9	4.9	•
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	Score	40	37	36	36	34	34	34	33	32.5	32	32	32	32	32	32	31	31	31	31	30.5	30	30	30	30			30	•
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hypothetical protein CP0296 [imported] - Chlamydophila pneumoniae (strain AR39)
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: H81592
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1466, 2000
A; Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255; PMID:10684935
A; Accession: H81592
A; Residues: 1-40 - REA>
A; Residues: 1-40 - REA>
A; Residues: 1-40 - REA>
A; Cross-references: UNIPROT:Q9KZA3; GB:AE002191; GB:AE002161; NID:g7189216; PIDN:AAF381E
C; Genetics:
A; Genetics:
A; Genetics:

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Gaps

.; 0

Query Match 18.4%; Score 37; DB 2; Length 40; Best Local Similarity 30.0%; Pred. No. 4.9e+02; Matches 6; Conservative 7; Mismatches 7; Indels

1 DSVTSTFSKLREQLGPVTQE 20

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Gaps

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Length 19;

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Crotoxin inhibitor 25K chain - tropical rattlesnake (fragment)
NyAlternate names: crotoxin inhibitor 23K chain (fragment)
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Accession: S74192; 867525
R;Perales, J.; Villela, C.; Domont, G.B.; Choumet, V.; Saliou, B.; Moussatche, H.; Bon, Eur. J. Biochem. 227, 19-26, 1995
A;Title: Molecular structure and mechanism of action of the crotoxin inhibitor from Crot A;Reference number: 867525; MUID:95154289; PMID:7851385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
Kseidues: 1-30 <PB2>
C;Superfamily: Crotalus neutralizing factor; Ly-6 homology
C;Keywords: glycoprotein; phospholipase A2 inhibitor
                                                                                                                                                          16.9%; Score 34; DB 2; I 31.2%; Pred. No. 4.8e+02; tive 6; Mismatches 5;
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    A;Molecule type: protein
A;Residues: 1-19 <SWE>
A;Cross-references: UNIPROT:Q7M4J1
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Best Local Similarity 33.3%;
Matches 6; Conservative
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                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             C. Accession: G84147
R. Takahi, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
R. Takani, H.; Nakasone, K.; Takahi, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4317, 2000
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A. Reference number: A83650; MUD: 20512582; PMID: 11058132
A. Accession: G84147
A. Reference preliminary
A. Molecule type: DNA
A. Residue: 1-34 STO.
A. Residue:
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A.Tile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A.Reference number: AB1807; MUID:2159285; PMID:11759840
A.Rccession: AH1838
A.Statuse preliminary
A.Molecule type: DNA
A.Residues: 1-35 < KUR>
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A,Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:Q9K5V4; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB077
A,Experimental source: strain C-125
C,Genetics:
A,Gene: BH3983
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C;Species: Aplysia californica (California sea hare)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B60977
E;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A;Title: Development of a database of amino acid sequences for proteins identified and A;Accession: B60977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytochrome c6 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2011 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1838
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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                                                                                                                                                                                                       hypothetical protein BH3983 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C,Date: 01-Dec-2000 #secuence revision 01-Dec-2000
                                                                                                                                                                                                                                                                            Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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85.7%; Pred. No. 5.5e+02;
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13 ESLGSTLSRAPSEISPIPEE 32
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Matches 8; Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Gene: petJ
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Gaps

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Length 30,

DB 2; Leny. . 8.1e+02;

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hypothetical protein 40c - Japanese black pine chloroplast
C;Species: chloroplast Pinus thunbergiana (Japanese black pine)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07516
R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-40 <WAK>
A;Residues: UNIPROT:Q32970; EMBL:D17510; NID:g529643; PIDN:BAA04394.1; PID:g1262
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A.Molecule type: protein
A.Residues: 1-31 <LON>
A.Cross-references: UNIPROT:P27687
C.Comment: This myohemerythrin is a monomeric oxygen-binding protein found in the retractive oxygen carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tubulin alpha chain, brain-specific isotype (clone pTUB6) - chum salmon (fragment)
Cispecies: Oncorhynchus keta (chum salmon)
Cibate: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 10-Jul-1998
CiAccession: C56635
R;Coe, I.R.; Munro, R.; Sherwood, N.M.
R,Coe, I.S.; Munro, R.; Sherwood, N.M.
A;Title: Isolation of different brain-specific isotypes of alpha-tubulins from chum salmAseq. A;Reference number: A56615; MUID:93208376; PMID:1296820
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A;Accession: A54257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
predicted
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                    ß.
R;Long, R.C.; Zhang, J.H.; Kurtz Jr., D.M.; Negri, A.; Tedeschi, G.; Bonomi, submitted to JIPID, April 1992
A;Reference number: JS0678
A;Accession: PS0350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Note: sequence extracted from NCBI backbone (NCBIN:128392, NCBIP:128391) C;Superfamily: tubulin P;28/Binding site: polyglutamate (Glu) (covalent) #status predicted F;33-34/Cleavage site: Glu-Tyr (tubulin-specific carboxypeptidase) #status F;33-34/Cross-link: peptide (Glu-Tyr) (by tubulin-tyrosine ligase) #status
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A;Note: sequence extracted from NCBI backbone (NCBIP:146748)
C;Superfamily: Lactobacillus acidophilus deoxyadenosine kinase
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Pred. No. 1.78+03;
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Pred. No. 1.6e+03;
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Pred. No. 1.5e+03;
3; Mismatches 4;
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28.6%;
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Best Local Similarity 39.1%;
Matches 9; Conservative
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Best Local Similarity 50.0%;
Matches 7; Conservative
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A,Molecule type: protein
A,Residues: 1-35 <IKE>
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Best Local Similarity
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A;Residues: 1-34 <COE>
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A; Status: preliminary
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A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
Brishmeson, A.JG.; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H. Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajian, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; F.G.; Nunes, L.S.; Oliveira, M.A.; de Soliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Salmsen, A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.R.; A.R.;
                                                                          Cispecies: Xylella fastidiose imported Ayeria rastrinosa (strain 3950)
Cispecies: Xylella fastidiose cevision 20-Aug-2000 #text_change 09-Jul-2004
Cidate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
Cidate: 18-Aug-2000 #sequence cevision 20-Aug-2000 #the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
Airitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Airitle: The genome sequence of the plant pathogen Xylella fastidiosa.
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C;Accession: PQ0844
B;Welters, P; Metz, B :; Fellx, G;; Palme, K.; Szczyglowski, K.; de Bruijn, F.J.
Plant Physiol. 102, 1095-1107, 1993
A;Title: Interaction of a rhizobial DNA-binding protein with the promoter region of a p;Accession: PQ0844; MUID:94105338; PMID:8278541
A;Accession: PQ0844
A;Molecule type: protein
A;Residues: 1-27 *WEL.
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C;Species: Phascolopsis gouldii
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                 hypothetical protein XP1988 [imported] - Xylella fastidiosa (strain
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C;Species: Azorhizobium caulinodans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
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Pred. No. 1.5e+03;
3; Mismatches 8; Indels
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Pred. No. 1.1e+03;
5; Mismatches 4;
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A;Experimental source: strain ORS571
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Best Local Similarity 38.9%;
Matches 7; Conservative
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Similarity 44.4%;
8; Conservative
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7 VGRNFARLRQEKG-LTQE
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Best Local Similarity
Matches 8; Conserv
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C;Date: 30-Jun-1992
C;Accession: PS0350
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8 셤 ò 셤

Gaps

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Length 40; 7; Indels

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A;Accession: C95169
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-40 <KUR>
A;Cross-references: UNIPROT:Q97PY5; GB:AE005672; PIDN:AAK75548.1; PID:g14972943; GSPDB:G-Status: 1-40 <KUR>
C;Genetics: A;Genetics: A;Genet
A; Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 32; DB 2; ilarity 41.2%; Pred. No. 2e+03; Conservative 3; Mismatches
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Best Local Similarity
Matches 7; Conserv
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Hypothetical protein NWA0180 [imported] - Neisseria meningitidis (strain 22491 serogroup c; Species: Neisseria meningitidis
C; Date: OS-Way-2000 #text_change 09-Jul-2004
C; Accession: B82012
R; Parkhill, J., A.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holrcyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID:20222556; PMID:10761919
A; Recession: B82012
A; Molecule type: DNA
A; Residues: 1-35 < PAR>
A; Coss-references: UNIPROT:Q9UWX5; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB8349
A; Experimental source: serogroup A, strain 22491
C; Genetics: NMA0180
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N.Alternate names: cysI protein homolog

S.Speciess: Vibrio cholerae

C.Speciess: Vibrio cholerae

C.Speciess: Vibrio cholerae

C.Speciess: Vibrio cholerae

C.SAccession: S70798

R.Camilli, A., Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A.Title: Use of recombinase gene fusions to identify Vibrio cholerae genes induced durin

A.Reference number: S70798; MUID:96414469; PMID:8817490

A.Accession: S70798

A.Status: preliminary; nucleic acid sequence not shown

A.Molecule type: DNA

A.Molecule type: DNA

A.Residues: 1-39 < CAM>
A.Residues: 1-39 < CAM>
A.Combinary; sulfite reductase
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Pred. No. 1.7e+03;
2; Mismatches 3; Indels
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             4 TSTFSKLREQLGPVTQEFWDNLE 26
                                                                                      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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14 KYLEQFGPVSE 24
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listeria mo ceratitis c

drosophila bactrocera drosophila drosophila drosophila

Q9mi02 Q9mi04 Q9mi06

dacus cilia ceratitis c

dacus

bactrocera

Run on:

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Sriranganathan N., Whichard J.M., Pierson F.W., Kapur V., Weigt L.A.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AR320576; AQQ14805.1; -.
Hypochetical protein.
SEQUENCE 37 AA, 4308 MW; 551EF5EA0BAAOCAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Engrailed (Fragment).
Pepsis sp. MFW-2001.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whiting M.F.;
Whiting M.F.;
Whiting M.F.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; AR275780; AAL35008.1; -.
GO; GO:0003700; F: transcription factor activity; IEA.
GO; GO:0003700; F: transcription of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR001057; Homeodomain_like.
PF00046; Homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                    Length 37;
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Last annotation update)
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Pred. No. 54
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Q9M102
Q9M104
Q9M104
Q9M124
Q9M124
Q9M124
Q8LYB3
Q8LYB9
Q8LYB9
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38.2%;
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                                                                                                                                                                                                                                                   Hypothetical protein.
Bacteriophage Felix 0
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NCBI_TaxID=173816;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=77775;
 05-JUL-2004
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01-MAR-2002
  Viruses:
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8WTG3;
                                                                                                                                                                                                              Q6KGF3;
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                                                                                                                                                                                                    O6KGF3
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Q8WTG3
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Q6KGF3
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QBwEg3 pepsis sp.
QBwEg3 bedcillus ce
Aas39602 baccillus ce
Aas39602 baccillus
G53103 rhodobacter
Q9mL26 drosophila
Q9ml26 drosophila
Q9ml26 drosophila
Q9ml26 drosophila
Q9ml36 drosophila
Q8lvv6 bactrocera
Q8lv6 anastrepha
Q7r3a plasmodium
Q9ml00 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                          26kgf3 bacteriopha
                                                              December 21, 2004, 12:02:34; Search time 189 Seconds (without alignments) 118.728 Million cell updates/sec
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Compugen Ltd.
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          GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Q8WTG3
Q8WT10
Q73DP3
AAS39602
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QBLYC8
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Q53103
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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length: 41
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02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 04-MAY-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
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                                                                                                                                                                          Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=222523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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02-MAR-2004 (
02-MAR-2004 (
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SEQUENCE 32
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                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                   AAS39602
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Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Cephoidea; Cephidae; Cephus.
NCBI_TaxID=173785;
                                                                                                                                                        1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                 22.6%; Score 45.5; DB 2; Length 39; 42.9%; Pred. No. 3e+02; tive 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45.5; DB 2; Length 39; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=222523;
                                                                           4687 MW; 42A28CCE81441488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 AA; 4687 MW; 42A28CCE81441488 CRC64;
                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Engralied (Fragment).
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05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last annotation update)
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                                                                                                                                                                                            12 EQLGPVTQEFWDNLEKETEGLRQEMSKD 39
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PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON TER 1
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PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
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InterPro; IPR009057; Homeodomain_like
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llarity 42.9%;
Conservative
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OrderedLocusNames=BCE0669;
                                                                                                     Query Match
Best Local Similarity 42.99
Marches 12; Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
                                                       39
39 AA;
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Q8WTIO;
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Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angluoll S.V., Kolonay J.F., Nolson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOI."; Nucleir Acids Res. 32:977-988(2004).
EMBL; AEGOGGS;
ATCC 10987 reveals metabolic to Bacillus anthracis pXO1.";
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HBu M.H., Chirala S.S., Makil S.J.;
Hwan fatty-acid synthase gene. Evidence for the presence of two
promoters and their functional interaction.";
J. Biol. Chem. 271:13584-13592(1996).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                    Length 32;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 protein.
32 AA; 3619 MW; C9161226273EB94C CRC64;
                                                                                                                                  Complete proteome, Hypothetical protein.
SEQUENCE 32 AA; 3619 MW; C9161226273EE94C CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acid synthase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 Score 45; DB 2;
Pred. No. 2.8e+02;
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"The genome sequence of Bacillus cereus adaptations and a large plasmid related Nucleic Acids Res. 32:977-988(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                            EMBL; AE017266; AAS39602.1; -. TIGR; BCE0669; -.
                                                                                                                                                                                                                      22.4%;
39.3%;
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Gaps

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29 AA

Length 40; 10; Indels

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y10771; CAA71745.1; -...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO01356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.5; DB 2; Length 29;
Pred. No. 1.2e+03;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lu J.X.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-1996).1; -. MPBJ 619.1; -. MPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wedeen C.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                              40 AA; 4849 MW; 21FA6215B27D5232 CRC64;
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Last annotation update)
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Last annotation update)
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Pred. No. 1.5e+03;
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29.2%; Pred. No. 1...
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      GO; GO:0006955; P:immune response; IEA.
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                           InterPro; IPR000353; MHC II beta.
Pfam; PF00969; MHC II beta; 1.
ProDom; PD000328; MHC II beta; 1.
Glycoprotein; MHC II; Transmembrane.
NON TER 1 1
NON_TER 40 40
SEQUENCE 40 AA; 4849 MW; 21FA6215B
                                                                                                                                                                                                                                                                                                                                                                                          13 QLGPVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                         :|| :|| |:|: | : :| |: 17 ELGRPDAEYWNRQKDEMDRVRAEL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA primase small subunit (Fragment)
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(TrEMBLrel. 03, I
(TrEMBLrel. 19, I
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                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
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01-DEC-2001
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045208
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Polvi A., Garden O.A., Batt R.M., Partanen J.;
Polvi A., Garden O.A., Batt R.M., Partanen J.;
Polvi A., Garden O.A., Batt R.M., Partanen J.;
Bublita AF041492; AAC0587.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0045012; F:MHC class II receptor activity; IEA.
GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
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MEDLINE=96062223; PubMed=7592416;
MEDLINE=96062223; PubMed=7592416;

Zeilstra-Ryalls J.H., Kaplan S.;

"Aerobic and anaerobic regulation in Rhodobacter sphaeroides 2.4.1:
the role of the fint gene.";
D. Bacteriol. 177:6422-6431(1995).
EMBL; U35445; AAC43501.1;
NON_TER
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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                                                                                                                                                                                                        Query Match 21.4%; Score 43; DB 2; Length 41; Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 2; Length 32;
Pred. No. 8.6e+02;
2; Mismatches 11; Indels
                                                                                                                                                   41 AA; 4668 MW; ECA60F116AB6E729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 32 AA; 3543 MW; 28D4595324F75D87 CRC64;
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Last annotation update)
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
InterPro; IPR000794; Ketoacyl_synth.
Brai; PF00109; ketoacyl-synt; 1.
NON_TER 41
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Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                19 QEFWDNL 25
                                                                                                                                                                                                                                                                                                                                                                        20 QEFWDNL 26
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                                                                                                                                                SEQÜENCE
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36 AA

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PubMed=12927135
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Q9MI20
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Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
Macroevolutionary relationships of species of Drosophila melanogaster group based on mtDNA sequences.";
Mol. Phylogenet. Evol. 28:518-528(2003).
EMBJ, AP164556; AAF81402.1;
Flybase; Psgn0042070; Dele\mt.Cyt-b.
GO: GO:005739; C:mitochondarion; IEA.
                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                      Mitochondrion.

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                               19.7%; Score 39.5; DB 2; Length 36; 39.3%; Pred. No. 1.5e+03;
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                                                                                                                    IndelB
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                                                                            36 AA; 4478 MW; E803EA629E459B67 CRC64;
                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b [Fragment).
Name=mt:Cyt-b; Synonyms=cytb;
Drosophila elegans (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TW-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
Name=mt.Cyt-b; Synonyms=cytb;
Drosophila eugracilis (Fruit fly).
Mitochondrion.
                                                                                                                                                                                                                     27 AA.
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                                                                                                                     6; Mismatches
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                                                                                                                                           12 EQLGPVTQEFWDNLEKETEGLRQEMSKD 39
                                                                                                                                                       3 EQLQRLKKEFQEN-RYLTEKRRQDLAND 29
InterPro; IPR009057; Homeodomain_like. Pfam; PF00046; Homeobox; 1. PRINTS; PR00024; HOMEOBOX. PROSITE; PS50071; HOMEOBOX 2; 1. DNA-binding; Homeobox; Nuclear protein.
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                                                                                                         Best Local Similarity. 39.3
Matches 11; Conservative
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14 INPLVSKWWDNL 25
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Best Local Similarity
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SEQUENCE FROM N.A.
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Q9MHZ4
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Kastanis P., Bilopoulos E., Goulielmos G.N., Teakas S., Loukas M.;
Kastanis P., Bilopoulos E., Goulielmos G.N., Teakas S., Loukas M.;
"Macroevolutionary relationships of species of Drosophila melanogaster
group based on mtDNA sequences.",
Mol. Phylogenet. Evol. 28:518-528 (2003).
EMBL, AFI04594; AAF81398.1,
Physae, Regn0042053) Difc.\mt.cyt-b.
GO:0005739; C:mitochondrion; IEA.
Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
"Macroevolutionary relationships of species of Drosophila melanogaster
group based on mtDNA sequences.";
Mol. Phylogenet. Evol. 28:18=528(2003).
EMBL, AF164595; AAF81400.1; --. EMBL, AF164595; AAF81400.1; --. G.S. GO:0005739; C:mitochondrion; IEA.
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                 Length 27;
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Pred. No. 1.2e+03;
4; Mismatches 3; Indels
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Pred. No. 1.2e+03;
4; Mismatches 3; Indels
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NON TER
1 1 1 SEQUENCE 27 AA; 3300 MW; D772900B035C3C18 CRC64;
                                                                                                                                                                                                                                          SEQUENCE 27 AA; 3300 MW; D772900B035C3C18 CRC64;
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
Name=mt:Cyt-b; Synonyms=cytb;
Drosophila ficusphila (Fruit fly).
Mitochondrion.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AA
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Drosophila kikkawai (Fruit fly).
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14 INPLVSKWWDNL 25
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                                                                   Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
"Macroevolutionary relationships of species of Drosophila melanogaster group based on mtDNA sequences.";
Mol. Phylogenet. Evol. 28:1518-528(2003).
EMBL; AF165580; AAF81370.1; -.
FlyBase; FBGN0042077; Daur\mt:Cyt-b.
GO: GO:0005739; C:mitochondrion; IEA.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Name=mt:(St-b): Synonyma=cytb;
Drosophila auraria (Fruit fly).
Mitochondrion.

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19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels
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19.4%; Score 39; DB 2; Length 27;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels
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NON TER 1 1 SEQUENCE 27 AA; 3313 MW; CD5B900B1530EC18 CRC64;
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27 AA; 3313 MW; CD5B900B1530EC18 CRC64;
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14 INPLVNKWWDNL 25
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14 INPLVNKWWDNL 25
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PubMed=12927135;
                                                       SEQUENCE FROM N.A.
NCBI_TaxID=30033;
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SEQUENCE
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Search completed: December 21, 2004, 12:18:24 Job time : 192 secs

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December 21, 2004, 12:05:32; Search time 151 Seconds (without alignments) 92.652 Million cell updates/sec
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1 DSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKD 39
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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	Description	Abp57175 Breast ca	7			2 Lecith	Aay19006 Lecithin:	Aay19260 Lecithin:	Aay18489 Lecithin:	9 Apo]	н	0 Mous	2 Antiox	Adc29658 Antioxida	Adc29661 Antioxida	Adc29657 Antioxida	Adc29659 Antioxida	Adc29660 Antioxida	Adc29669 Antioxida	Adc29665 Antioxida	Adc29668 Antioxida	Adc29670 Antioxida	Adc29664 Antioxida	Adc29667 Antioxida	Adc29666 Antioxida	Aar48545 Sequence
SUMMARIES	QI	ABP57175	AAG62607	AAE02141	AAU99633	AAY18752	AAY19006	AAY19260	AAY18489	ADG20969	ADJ32911	ADP80870	ADC29662	ADC29658	ADC29661	ADC29657	ADC29659	ADC29660	ADC29669	ADC29665	ADC29668	ADC29670	ADC29664	ADC29667	ADC29666	AAR48545
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compositions comprising: (a) a BPI, or a nucleic acid encoding a BPI, and a carrier; or (b) the antibody of (1), or a fragment or derivative of the antibody, and a carrier; or (1) screening for agents that interact with one or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion or proteins; (4) screening for or identifying agents that modulate the expression or activity of one or more BPIs, a BPI fragment, a BPI-related to Polypeptide, or BPI-fusion proteins; and (5) treating or preventing compression or activity of one or more BPIs, a BPI fragment, a BPI-related to Polypeptide, or BPI-fusion proteins; and (5) treating or preventing complements. The range or severity of one or accreening, diagnosing or determining the strength or severity of breast cancer, identifying a subject at risk of developing breast cancer, or monitoring the effect of therapy or developing breast cancer, or monitoring the effect of therapy or administered to a subject with breast cancer. The antibodies the activity of one or more BPIs are useful for treating or preventing breast cancer. ABBF3104 to ABBF320 represent breast cancer associated tryptic digest peptides, which are useful for treating or preventing breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel oxidized form of apolipoprotein useful in diagnosis and treatment of diseases associated with oxidative stress such as cardiovascular diseases, in particular, atherosclerosis.
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100.0%; Prev
0; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein fragment #1.
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                Sequence 16 AA;
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Modified-site
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The present invention relates to oxidised apolipoprotein A-I (ApoA-I) where at least Met residue 86 is oxidised to Met(O). This can be used in the prevention, diagnosis and treatment of lipid associated disorders,

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including coronary vascular disease, ischaemic heart disease, atherosclerosis and dyslipidaemias. The present sequence is a fragment of the ApoA-I protein isolated in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is mouse alpha helical protein-34 (Zalpha34) artigenic epitope. Zalpha34 polymucleotides, polypeptides and antibodies are useful as educational tools, as a laboratory practicum kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. Zalpha34 is useful for promoting entibodies that specifically binds to Zalpha34 groups, peptides or polypeptides. The antibodies are useful for inhibiting spermatogenesis and to isolate DNA sequences that encode human Zalpha34 genes from cDNA libraries. Zalpha34 polypeptides are useful as an aid to teach preparation of antibodies, identifying proteins by western blotting, protein purification and determining the weight of expressed Zalpha34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides as a ratio to total protein expressed. Fusion proteins comprising Zalpha34 and a Fc group are useful as an in vitro assay tool and antibody-Zalpha34 fusion comprising antibody variable domains are useful as therapeutic proteins, in which the antibody group binds with the target antigen, such as a tumour associated antigen
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Educational kit useful for courses related to genetics, molecular biology, protein chemistry, antibody production and analysis, has a container having novel alpha helical protein-34 polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                   Mouse alpha helical protein-34 (Zalpha34) antigenic epitope #12
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse, alpha helical protein-34; Zalpha34; antiinfertility, antigenic epitope, spermatogenesis, educational kit; therapy; tumour associated antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.1%; Score 60.5; DB 4; Length 37;
                                                                                      , DB 4; Le...
                                                                                                                                    Mismatches
                                                                                                    Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                              AAE02141 standard; peptide; 37 AA.
                                                                                                       39.c.
100.0%; Fi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 66; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2000; 2000WO-US029277.
                                                                                                                                                                          38
                                                                                                                                                                                                 DNLEKETEGLRQEMSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00430153
                                                                                                      39.88;
                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2001 (first entry)
                                                                                                                                                                          DNLEKETEGLROEMSK
                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conklin DC, Taft DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-316446/33.
                                                                     Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200132884-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2001.
                                                                                                                                                                                                                                                                                                                              AAE02141;
                                                                                                                                                                          23
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                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                              AAE02141
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The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 14-22 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at
                                                                                                                                                                                                            Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia; cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I; high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists
                                                                                                                                                                        Lecithin:cholesterol acyltransferase activation exhibiting peptide #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%; Score 56; DB 2; Length 22; 42.9%; Pred. No. 3.9; ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornut I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide agonists of apolipoprotein A-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 107; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY19006 standard; peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buttner K,
                                          AAY18752 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PVLDEFWEKLNEXLEALKOKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00940093.
                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dasseux J, Sekul R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-277031/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEKUL R.
BUTTNER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DASSEUX J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORNUT I.
METZ G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1997;
                                                                                                                             09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               WO9916408-A2
                                                                                                                                                                                                                                                                                                        septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-1999.
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                                                                                     AAY18752;
                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (METZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BUTT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
AAY19006
  RESULT 5
                          AAY18752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SXXXE
                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an educational kit or aid for teaching protein chemistry comprising a container having the isolated, novel hormonal/

C cytokine alpha helical protein 34 (secreted protein alpha, 2alpha34)

polypeptide, comprising defined amino acid sequences (AAU99639-AAU99654)

given in the specification and/or the isolated polypeptides comprising

(AAU99639-AAU99654). The educational kit or teaching aid may be used to teach protein chemistry. A novel full-length Zalpha34 protein can be used so the student can have practical learning experiences in protein procedures, protein re-folding when the protein is produced in proxaryctic host cells, and how to make both monoclonal and polyclonal antibodies. Antibodies that bind to mature Zalpha34 proteins can also be used to learn how to make both monoclonal and polyclonal antibodies. Antibodies affinity purification columns, to do enzymetinked immunoabsorbent assays (ELISA). The mouse gene encoding Zalpha34 is located on chromosome 7. Zalpha34 is useful for promoting spermatogenesis. The present sequence is an immunogenic epitope from the mouse Zalpha34 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Educational kits and aid for teaching protein chemistry comprising the isolated hormonal/cytckine cytokine alpha helical protein-34 (Z alpha 34) polypeptide, useful for teaching e.g. ELISA techniques and immunopurification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Mouse; secreted alpha protein 34; Zalpha34; epitope; immunogen; chromosome 7; spermatogenesis; hormonal; cytokine; teaching aid; protein chemistry; enzyme-linked immunoabsorbent assay; ELISA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                        Indels
                                                                                                                                                                                                                                                                                                                                                Mouse secreted alpha protein 34, Zalpha34, epitope #12.
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  Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 51-52; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 EQLGPVTQEFWDNLEKETEGLRQE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| | |||||:|| : ||:|
EELGE-AQTVWDNLQKELDLLREE 23
                                                              12 EQLGPVTQEFWDNLEKETEGLRQE 35
                                                                                       AAU99633 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2000; 2000US-00695458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0162623P
54.28;
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 54.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taft DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-526165/56.
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6380361-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-1999;
                                                                                                                                                                                                                                                                                                   07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2002
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                      Matches
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Metz G;

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Gaps

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09-JUL-1999 (first entry)

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98WO-US020327. 97US-00940095

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SEKUL R.
BUTINER K.
CORNUT I.
METZ G.
                                                                                                                                                                                                                                                                                                                      DUFOURCO J.
                                                                                                                                                                                                                                DASSEUX J.
septic shock.
                                                     Homo sapiens.
                                                                                                                                                            28-SEP-1998;
                                                                                                                                                                                             29-SEP-1997;
                                                                                      WO9916459-A1
                                                                                                                         08-APR-1999.
                                 Synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY18489;
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                                                                                                                                                                                                                                (DASS/)
(SEKU/)
                                                                                                                                                                                                                                                                                                                      (DUFO/)
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AAY18489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (apoA-1) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atheroscierosis, restenosis, HDL (high density lipoprotein) or apoA-1 deficiency; hypertriglyceridemia and metabolic syndrom, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also too image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to AAY19187 represent legithin; cholesterol acyltransferase (LCAT) activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human; lecituln:cholesteerol acyltransferase; LCAT; hypercholesterolaemia; cardicovascular disease; atherosecleroseis; restenosis; HDL; apoA-I; high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
                                               Apolipoprotein A-1; agonist; dyslipidemic disorder; dyslipidemia; human; lecithin:cholesterol acyltransferase; LGAT; hypercholesterolaemia; cardiovascular disease; arberosclarosis; restenosis; HDL; apoA-1; high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lecithin: cholesterol acyltransferase activation exhibiting peptide #73.
              Lecithin:cholesterol acyltransferase activation exhibiting peptide #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an agonist (A) of apolipoprotein A-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metz G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exhibiting core peptides, which are apoA-I agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornut I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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42.9%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide agonists of apolipoprotein A-I.
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                                                                                                                                                                                                                                                                                                                  97US-00940096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dasseux J, Sekul R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-277034/23
                                                                                                                                                                                                                                                                                                                                                     DASSEUX J.
SEKUL R.
BUTTNER K.
CORNUT I.
                                                                                                                                                                                                                                                                                                                                                                                                           CORN/) CORNUT METZ G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 AA;
                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                             WO9916458-A1
                                                                                                                                                                                                                                                                                                                    29-SEP-1997;
                                                                                                                                                                                                                                                                                   28-SEP-1998;
                                                                                                                       septic shock
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                                                                                                                                                                                                                                              08-APR-1999
                                                                                                                                                          Synthetic
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(SEKU/)
(BUTT/)
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Gene therapy, apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT; hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
                                                                                                                                                                                              The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia am metabolic syndrome, also for treating septic shock. When labeled (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to Image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to AAY1941 represent lecithin-cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lecithin: cholesterol acyltransferase activation exhibiting peptide #73.
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  Dufourcq J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 56; DB 2; Length 22;
42.9%; Pred. No. 3.9;
tive 5; Mismatches 7; Indels
  Metz G,
Cornut I,
                                                                                                  Peptide agonists of apolipoprotein A-I.
                                                                                                                                                    Example; Page 119; 280pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY18489 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
Dasseux J, Sekul R,
                                               WPI; 1999-277035/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9916409-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1999.
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Dufourcq J;

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Novel apolipoprotein agonist treating subject suffering from disorder associated with dyslipidemia such as hypercholesterolemia, cardiovascular disease, atherosclerosis, restenosis, hypertriglyceridemia or metabolic syndrome.
                                                                                                                                                                                                                                                                                                                 The invention describes an apolipoprotein A-I (ApoA-I) agonist (A) comportsing a 15-29 residue peptide or peptide analogue which forms an amphipathic alpha-helix in the presence of lipids or its salt. (A) is useful for treating a subject suffering from a disorder associated with dyslipidaemia (hypercholesterolaemia, cardiovascular disease, atherosclaerosis, restenosis, high density lipoprotein (HDL) or Apia-I deficiency, hypertriglyceridaemia or metabolic syndrome) or septic shock this is the amino acid sequence of a ApoA-I agonist peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dyslipidaemia; hypercholesterolaemia; cardiovascular disease; atherosclerosis; restenosis; high density lipoprotein deficiency; HDL deficiency; hypertriglyceridaemia; metabolic syndrome; septic shock; coronary heart disease; endotoxaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo lipoprotein A-I agonist; ApoA-I agonist; amphipathic alpha-helix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 56; DB 8; Length 22; 42.9%; Pred. No. 3.9;
                                                                                                                 Cornut I, Metz G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo lipoprotein A-I (ApoA-I) agonist peptide #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                Claim 19; SEQ ID NO 73; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ32911 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buttner K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-MAR-2002; 2002US-00099574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00465718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Aib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                               Dasseux J, Sekul R,
SEKUL R.
BUTTNER K.
CORNUT I.
METZ G.
DUFOURCQ J.
                                                                                                                                                    WPI; 2004-010524/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKUL R.
BUTTNER K.
CORNUT I.
METZ G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DASSEUX J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003060604-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ32911;
                                      (CORN/) (METZ/) N(DUFO/) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DASS/) 1
(SEKU/) (
(BUTT/) 1
(CORN/) (
(METZ/) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc?
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                        applipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog, which forms an amphipathic alpha-helix in presence of lipids. (A), optionally as a complex with lipids, and host cells that contain (A), are useful for gene therapy, or prevention, of diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I efficiency, hypertriglyceridemia and metabolic syndrome, also to treat endotoxemia (septic shock). Host cells containing (A) can also be used to study the role of apoA-I in lipid metabolism. (B) can be used diagnostically, e.g. to measure serum HDL (particularly its subpopulation involved in retrograde cholesterol transport) and for imaging the circulatory system or HDL accumulations at fatty streaks. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein A-I; ApoA-I; agonist; peptide analogue; amphipathic alpha-helix; dyslipidaemia; hypercholesterolaemia; cardiovascular disease; atherosclerosis; restenosis; high density lipoprotein; HDi; Apia-I deficiency; hypertriglyceridaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                            Dufourcq
                                                                                                                                                                                                                                                                                                                                                                            present invention describes a nucleic acid (A) encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 56; DB 2; Length 22; 42.9%; Pred. No. 3.9; 7; Indels ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a peptide from the present invention
                                                                                                                                                                                                                            Metz G,
                                                                                                                                                                                                                                                                                                  Nucleic acid encoding apoproteinA-I agonist peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apolipoprotein A-I agonist peptide seq id 73.
                                                                                                                                                                                                                            Cornut I,
                                                                                                                                                                                                                                                                                                                                     Example; Page 148; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PVLDEFWEKLNEXLEALKOKL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG20969 standard; peptide; 22 AA
                                                                                                                                                                                                                          Buttner K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metabolic syndrome; septic shock
                     98WO-US020329.
                                                        97US-00940136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2002; 2002US-00099836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00453834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                          Dasseux J, Sekul R,
                                                                                                           SEKUL R.
BUTTNER K.
CORNUT I.
METZ G.
                                                                                                                                                                                                                                                               WPI; 1999-254921/21
                                                                                                                                                                                     DUFOURCO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                             DASSEUX J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DASS/) DASSEUX J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003203842-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1999;
                   28-SEP-1998;
                                                        29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG20969;
                                                                                                                                                                 (METZ/)
(DUFO/)
                                                                                                                                (BUTT/)
                                                                                                               SEKU/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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7; Indels

Gaps

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The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
          of a protein with c-foss protein; and (4) detecting (MII) the interaction of a protein with c-foss protein; and (4) detecting (MII) the interaction protein as mentioned in (3) with c-fos protein, by contacting the protein with c-fos, to form a complex. (MI) is useful for detecting its interaction with c-fos, to form a complex. (MI) is useful for screening the protein that interacts with c-fos which involves performing the cheetcrion process and selecting the protein that interacts with c-fos. (MI) is useful for screening inhibitors that interact with c-fos which involves performing (MI) and selecting the detected protein. (I) is useful for screening inhibitors that interact with c-fos which can interact with c-fos which can interact with c-fos in the exemplification of the present invention.
with c-fos protein; (3) an inhibitor (IV) that inhibits interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cysteine-containing peptides, having antioxidant properties, useful for diagnosing and treating cardiovascular disease, ischemia, bone disease and other inflammatory related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular disease; ischaemia; bone disease; related disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.9%; Score 52; DB 7;
100.0%; Pred. No. 10;
ive 0; Mismatches
                                                                                                                                                                                                                                                .
8
                                                                                                                                                                                                                                                DB 8
                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; SEQ ID NO 37; 49pp; English
                                                                                                                                                                                                                                                                                                                 31
                                                                                                                                                                                                                                                                                                                                    :| |||||| :|
ELEBQLGPVAEETRARLGKEEQG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC29662 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                 KLREQLGPVTQEFWDNLEKETEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2002; 2002US-00142238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-2001; 2001US-0289944P.
                                                                                                                                                                                                                                                27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                               Local Similarity 52.2
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antioxidant peptide #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DSVTSTFSKLR 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIEL/) BIELICKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003087819-A1.
                                                                                                                                                                                                                 Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antioxidant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bielicki JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC29662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADC29662
88888888888888888888
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                                                                                                                                                                           The invention comprises Apo lipoprotein A-I (ApoA-I) agonist peptides which form an amphipathic alpha-helix in the presence of lipids. The ApoA-I peptides of the invention are useful for treating a disorder associated with dyslipidaemia, such as: hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, high density lipoprotein (HDL) deficiency, ApoA-I deficiency, hypertriglyceridaemia, metabolic syndrome, and septic shock. The ApoA-I peptides are also useful for treating coronary heart disease and endotoxaemia. The present amino acid sequence represents an ApoA-I agonist peptide of the invention.
                                                             New Apo lipoprotein A-I agonist useful for treating disorders associated with dyslipoproteinemia e.g. hypercholesterolemia orseptic shock, comprises 15-29 reside peptide or analog which forms amphipathic alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
££
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-fos; c-fos interacting protein; fos interacting protein chromosome X; Fip-cx; screening; Fc-fos interacting protein inhibitor; mouse; apoliloprotein E.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a protein (I) that interacts with c-(e.g., fos interacting protein chromosome X (Fip-cx), Fip-ox.1, fos interacting protein chromosome ex.2, or fos interacting protein chromosome 4). Also described: (1) unucleic acid (II) that encodes (2) an inhibitor (III) that inhibits the interaction of (I) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fos interacting protein
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 22
                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse apolipoprotein E amino acid sequence SEQ ID NO:95.
ö
 Metz
Cornut I,
                                                                                                                                                                                                                                                                                                                                                                                                  3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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                                                                                                                                                Example 8; SEQ ID NO 73; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 89; SEQ ID NO 95; 192pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                               27.9%; Score 56; 42.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yanagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP80870 standard; peptide; 31 AA.
Buttner K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-2003; 2003WO-JP014749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-DEC-2002; 2002JP-00360046
                                                                                                                 helix in presence of lipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishizaka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fip-cx)
Sekul R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-517250/49.
N-PSDB; ADP80934.
                                WPI; 2004-059110/06
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYKE-) UNIV KEIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004053121-A1
                                                                                                                                                                                                                                                                                                                                                Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyamoto E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-2004
 Даввецх J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP80870;
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ADP80870
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The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
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                                                                                                                                                                          New cysteine-containing peptides, having antioxidant properties, useful for diagnosing and treating cardiovascular disease, ischemia, bone
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antioxidant; cardiovascular disease; ischaemia; bone disease; inflammatory related disease; human.
                                                                                                                                                                                                                                                                                                                                                      25.9%; Score 52; DB 7; Length 18; 100.0%; Pred. No. 10; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                      disease and other inflammatory related diseases.
                                                                                                                                                                                                                             Example 8; SEQ ID NO 36; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; SEQ ID NO 32; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC29657 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                        25.95,
100.0%; Pre-
                                                    08-MAY-2002; 2002US-00142238
                                                                           09-MAY-2001; 2001US-0289944P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002; 2002US-00142238.
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                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antioxidant peptide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 DSVTSTFSKLR 11
                                                                                                   (BIEL/) BIELICKI J K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIEL/) BIELICKI J K.
                                                                                                                                                    WPI; 2003-786946/74.
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003087819-A1
   US2003087819-A1
                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                           Bielicki JK;
                           08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2003.
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ADC29657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
                                                                                                                                                                                                                                                                                                                                                                                                                               New cysteine-containing peptides, having antioxidant properties, useful for diagnosing and treating cardiovascular disease, ischemia, bone disease and other inflammatory related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                            antioxidant, cardiovascular disease, ischaemia, bone disease, inflammatory related disease, human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antioxidant; cardiovascular disease; ischaemia; bone disease; inflammatory related disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 18;
10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC29661 standard; peptide; 18 AA.
                                                                          ADC29658 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                               09-MAY-2001; 2001US-0289944P
                                                                                                                           (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
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Antioxidant peptide #33
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                                                                                                                                                                                                                                                                                                                                                      (BIEL/) BIELICKI J K.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-786946/74.
                                                                                                                                                                                                                                                     US2003087819-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                           18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                               Bielicki JK;
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                                                                                                                                                                                                                 Synthetic
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                                                                                                   ADC29658;
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The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
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Sequence 18 AA;

ô Gaps ö Query Match 25.9%; Score 52; DB 7; Length 18; Best Local Similarity 100.0%; Pred. No. 10; Matches 11; Conservative 0; Mismatches 0; Indels

1 DSVTSTFSKLR 11 ò

8 DSVTSTFSKLR 18 쉽

Search completed: December 21, 2004, 12:21:51 Job time : 155 secs

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December 21, 2004, 11:55:11; Search time 142 Seconds (without alignments) 98.279 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBGOMB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ipt	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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		-20	37	-49	73	73	-73	73	US-10-099-836B-73	73	US-10-802-080-73	73	-59	-32
		JS-10-465-789A-50	JS-10-700-340-37	39A.	68	68	74A	6	36B	,-66	08	16	39A	JS-10-142-238A-32
ES		5-7	9-34	5-78	9-5	9-5	-5	7-87	9-8	3-5	2-0	1-8	5-7	2-2
SUMMARIES	į	46	-70(	-46	-86	-86	-09	-14.	-09	-28.	-80	-80	-46	-14
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ation 1004005 222222222222222222222222222222222	artif
AA-50  AA	TRYPORMATION: artificial set 789A-50  atch Samilarity 100.0%; P. 22; Conservative 0; 16 PVTOEFWDNLEKETEGLRQEMS 1 PVTQEFWDNLEKETEGLRQEMS 1 PVTQEFWDNLEKETEGLRQEMS
52 25.9 52 25.9 64 23.9 48 23.9 48 23.9 48 23.9 48 23.9 48 23.9 48 23.9 44 47 23.4 47 23.4 47 23.4 47 23.4 47 23.4 47 23.4 47 23.4 47 23.4 47 23.9 66 22.9 66 22.9 66 22.9 66 22.9 67 20.4 67 23.4 68 23.9 68 22.9 68	10 10 10 10 10 10 10 10 10 10 10 10 10 1
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Butther, Klaus
Cornut, Isabelle
Metz, Gunther, Sucher
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBSLEGQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: AUMNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB
Pred. No. 2.3;
Mismatches
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OTHER INFORMATION: Xaa = Aib
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: No. US20030008827Ale FEATURE:
                                                                                                                                                                                       Sequence 73, Application US/09865989
Publication No. USZ0030008827A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PVTQEFWDNLEKETEGLRQEM 36
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|PVLDEFWEKLNEXLEALKQKL 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-493-4935
TELERA: 650-493-5556
TELEX: 66141 PRINIE
INFORMATION FOR SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 42.9%;
Matches 9; Conservative
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                                         1 DSVTSTFSKLREQLG 15
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Conservative
  15;
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US-09-865-989-73
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Matches
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                                                                                                                                     TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREATILE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREATILE OF INVENTION: CANCER.

TITLE OF INVENTION: CANCER.

FILE REFERENCE: 2543-1-032

CURRENT FILING DATE: 2003-11-03

PRIOR APPLICATION NUMBER: US/10/700,340

PRIOR PLILNG DATE: 2001-05-02

PRIOR PLILNG DATE: 2001-05-02

PRIOR PLILNG DATE: 2001-07-27

PRIOR PLILNG DATE: 2001-07-27

PRIOR APPLICATION NUMBER: GB0118385.4

PRIOR PLILNG DATE: 2001-08-14

PRIOR PLILNG DATE: 2001-08-14

PRIOR PLILNG DATE: 2001-08-16

PRIOR PLILNG DATE: 2001-08-16

PRIOR PLILNG DATE: 2001-08-16

PRIOR PLILNG DATE: 2001-01-11-22

NUMBER OF SEQ ID NOS: 156

SOFTWARE: PATENTINY VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; L
6.7e-05;
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Publication No. US20040053384A1
GENERAL INFORMATION
APPLICANT: Sligar, Stephen G
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Yelena V. Grinkova
APPLICANT: Tila G Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

COTHER INFORMATION: artificial sequence of Helix

US-10-465-789A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.8%; Score 72; DB 15; 100.0%; Pred. No. 0.018;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT PILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
LENGTH: 23
                                                                              Sequence 37, Application US/10700340 Publication No. US20040203023A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EQLGPVTQEFWDNLEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 EQLGPVTQEFWDNLEK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-700-340-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 37
LENGTH: 16
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Sequence 73, Application US/10147849

Sequence 73, Application US/10147849

Publication No. US20030190319A1

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Bettner, Klaus

APPLICANT: Bettner, Klaus

APPLICANT: Metz, Gunther

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 254

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            009196-0005-999
                                                                                                                      STATE: NEW ACCES
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATION SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,574A
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REJECTOMONICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: No. US20030060606Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 PVTQEFWDNLEKETEGLRQEM 36
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) OTHER INFORMATION: Xaa = Aib

US-10-099-574A-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Other
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                                                                               Sekul, Kenate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APDLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 73. Application US/10099574A
Publication No. US20030060604A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: DISKETCE
COMPUTER: DISKETCE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: RESESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIPICATION: -CURNOWN:
RIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUYA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION IN
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 13
OTHER INFORMATION: Xaa = Aib
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: No. US20040029807A9e
                               GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 PVTQEFWDNLEKETEGLRQEM 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
Publication No. US20040029807A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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Gaps

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Sequence 73, Application US/10283599;
Publication No. US20030208059A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS:
NUMBER OF SEQUENCES: 274
CORRESPONDENCES: 274
APPLICANT: CORNESSIONUBLES OF SEQUENCES: ADDITIONAL OF SEQUENCES: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.9%; Score 56; DB 14; Length 22; Best Local Similarity 42.9%; Pred. No. 2.3; Matches 9; Conservative 5; Mismatches 7; Indels
         REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       009196-0007-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 13

; COTHER INFORMATION: Xaa = Aib

; SEQUENCE DESCRIPTION: SEQ ID NO: 73:

US-10-099-836B-73
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: No. US20030203842Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/283,599
FILING DATE: 29-OCT-2002
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the Americas CITY: New York
STATE: NY
COUNTY: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PVLDEFWEKLNEXLBALKQKL 21
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APPLICATION NUMBER: 08/940,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                   INFORMATION FOR SEQ 1D NO. 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELERAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-10-283-599-73
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US-10-099-836B-73
Sequence 73. Application US/10099836B
Publication No. US20030203842A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.9%; Score 56; DB 14; Length 22;
42.9%; Pred. No. 2.3;
tive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FRAESEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,836B

FILING DATE: 28-Aug-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: «Unknown»

PRILNG DATE: CUNKNOWN»

FILING DATE: CUNKNOWN»

ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, LAUFA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                       009196-0005-999
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/147,849
FILING DATE: 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: No. US20030190319Ale
                                                                                             CLASSIPECATION
CLASSIPECATION
PRIOR APPLICATION DATA:
APPLICATION UNDER:
FILING DATE:
FILING DATE:
ATTONEY/AGENT INFORMATION:
NAME: COLUZZI, LAULA A
REGISTRATION UNDER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00919
TELEPHONE: 650-493-4935
TELEFAN. 650-493-556
TELEFAN: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 PVTQEFWDNLEKETEGLRQEM 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-10-147-849-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9%
Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Other
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Gaps

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Gaps
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Publication No. US20040198662A1
GENERAL INFORMATION:
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Grant, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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                                                                                       Query Match 27.9%; Score 56; DB 16; Length 22; Best Local Similarity 42.9%; Pred. No. 2.3; Matches 9; Conservative 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 009196-0006-999
  OTHER INFORMATION: Xaa = Aib
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: IBM Compatible
COMPUTE: IBM Compatible
COPERATING SYSTEM: DOS
SOCTHARE: FEASTEN VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/801,897
FILING DATE: 15-Mar-2004
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-199
ATTORNEY/AGENT INFORMATION:
NAMME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                   16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                               1 PVLDEFWEKLNEXLEALKOKL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 PVTQEFWDNLEKETEGLRQEM 36
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-10-801-897-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino a
STRANDEDNESS:
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US-10-801-897-73
                                            US-10-802-080-73
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Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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                                                                                                                                                                                                                                                       DB 14; Length 22;
                                                                                                                                                                                                                                                                                               Indels
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MEDIUM TYRE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/802,080
FILING DATE: 15-Mar-2004
CLASSIPICATION: -Unknown>
PRIOR APPLICATION: -Unknown>
PRIOR APPLICATION NUMBER: US/09/453,840
FILING DATE: 01-DEC-1999
APPLICATION NUMBER: 08/940,095
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura A
REGISTRATION NUMBER: 30,742
REGERRENCE/DOCKET NUMBER: 09196-0004-999
TELEPHONE: 650-493-4935
TELEFRAN: 660-493-4955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                  Query Match 27.9%; Score 56; DB 1
Best Local Similarity 42.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches
                                                                                         MOLECULE TYPE: No. US20030208059Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 73, Application US/10802080 Publication No. USZO040181034A1 GENERAL INFORMATION: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                         16 PVTOEFWDNLEKETEGLROEM 36
                                                                                                                                                                                                                                                                                                                                                                        1 PVLDEFWEKLNEXLEALKOKL 21
                                                                                                                               NAME/KEY: Other
LOCATION: 13
COTHER INFORMATION: Xaa = Aib
US-10-283-599-73
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INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
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STRANDEDNESS: single
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 33, Application US/10142238A

Publication No. US20030087819A1

GENERAL INFORMATION:
APPLICANT: Bielicki, John K.
TITLE OF INVERTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REFERENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT FILING DATE: 2002-08-19
PRIOR PLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
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GENERAL INCRAMATION
GENERAL INCRAMATION
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REFERENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.9%; Score 52; DB 14; Length 18; Best Local Similarity 100.0%; Pred. No. 6.2; Matches 11; Conservative 0; Mismatches 0; Indels
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NAME/KEY: PEPTIDE
LOCATION: (1)..(18)
OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(18)
COTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-33
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; Sequence 34, Application US/10142238A
; Publication No. US20030087819A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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Matches 11; Conservative
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                                                                             US-10-142-238A-33
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US-10-142-238A-32
is Sequence 32, Application US/10142238A
is Sequence 32, Application No. US20030087819A1
is GENERAL INFORMATION:
is APPLICANT: Bielicki, John K.
is TITLE OF INVENTION: CSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
is FILE REFERENCE: IB-1705
is CURRENT FILING DATE: 2002-08-19
is PRIOR FILING DATE: 2001-08-19
is PRIOR FILING DATE: 2001-08-19
is NUMBER OF SEQ ID NOS: 84
is SOFTWARE: Patentin version 3.1
is SEQ ID NO 32
is LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: artificial sequence of Helix 0.5 US-10-465-789A-59
                                                                                             RESULT 12
US-10-465-789A-59
Sequence 59, Application US/10465789A
Publication No. US200400533441
GENERAL INPORMATION:
APPLICANT SIGAR, Stephen G
APPLICANT Schuler, Mary A
APPLICANT Civjan, Natamya R
APPLICANT Civjan, Natamya R
APPLICANT I Givjan, Natamya R
APPLICANT Schuler, Mary A
APPLICANT Fila G. Denisov
FILE REFERENCE: 87-00A
CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT FILING DATE: 2003-06-18
PRIOR FILING DATE: 2003-06-18
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
SPRIOR FILING DATE: 2000-11-20
SEQ ID NOS: 89
SECTION OS SEQ ID NOS: 89
SERVICE SERVICES SECTION OF SEQ ID NOS: 89
SERVICE SEQ ID NOS: 89
SERVICE SEQ ID NOS: 89
SERVICE SEQ ID NOS: 89
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COTATION: (1)..(18)
COTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-32
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 100.
Matches 11, Conservative
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13; Conservative
 TYPE: PRT ORGANISM: Mus musculis
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Best Local Similarity
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US-09-695-458-15
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                                                                                                                          December 21, 2004, 11:59:59; Search time 37 Seconds (without alignments) 69:903 Million cell updates/sec
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Sequence 73,
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-940-095-73
US-08-940-096-73
US-09-465-719-73
US-09-453-803-73
US-09-453-813-73
US-09-453-813-73
US-09-453-814-73
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US-08-940-095-75
US-08-940-095-75
US-08-940-096-75
US-09-455-719-75
US-09-453-838-75
US-09-940-136-75
US-08-940-136-75
US-08-940-136-75
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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seq length: 41
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ{\circ}{\circ}$\circ \circ \circ
                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                          OM protein
                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                              Run on:
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Sequence 15, Application US/09695458

Patent No. 6380361

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Taft, David W.
TITLE OF INVENTION: Educational Kit and Method Containing No. 6380361el Alpha Helical
TITLE OF INVENTION: Protein-34
FILE REFERENCE: 99-78
CURRENT APPLICATION NUMBER: US/09/695,458
CURRENT APPLICATION NUMBER: 60/162,623
PRIOR APPLICATION NUMBER: 60/162,623
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
   RESULT 2
US-08-940-095-73
US-08-940-095-73
Sequence 73, Application US/08940095
Sequence 73, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Descur, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
ITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
ITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
SCORESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                    Sequence Sequence
                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
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Sequence
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Pred. No. 0.27;
4; Mismatches 6;
US-09-453-833-75
US-09-453-826-75
US-09-865-989-75
US-09-453-834-75
US-08-940-095-120
US-08-940-096-120
US-08-940-096-120
US-09-453-838-120
US-09-453-838-120
US-09-453-838-120
US-09-453-838-120
US-09-453-838-120
US-09-453-841-120
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COMPUTER: DISKULCE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: PEASESQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PVTOEFWDNLEKETEGLROEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PVLDEFWEKLNEXLEALKOKL 21
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 00919
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-491-556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i LOCATION: 13
i OTHER INFORMATION: Xaa = Aib
US-08-940-093-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New
STATE: NY
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Sequence 73, Application US/08940093
Patent No. 6027323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Guncher
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.9%; Score 56; DB 3; Length 22; Best Local Similarity 42.9%; Pred. No. 0.58; Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    009196-0004-999
                          ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EN Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CORLUZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00919
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERAX: 650-493-5556
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-08-940-095-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: No. 6004925e
FEATURE:
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US-08-940-096-73

Sequence 73, Application US/08940096

Sequence 73, Application US/08940096

Sequence 73, Application US/08940096

Sequence 73, Application US/08940096

Sequence 73, Application

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

ITILE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 56; DB 3; ilarity 42.9%; Pred. No. 0.58; Conservative 5; Mismatches
009196-0006-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  009196-0005-999
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APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                 Length 22;
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                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FABSTEW Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/45,605
FILING DATE: 26-No. 6323341-1999
CLASSIFICATION NUMBER: 08/940,095
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE: -Uhknown>
APTICATION NUMBER: 08/940,095
FILING DATE: -Uhknown>
APTICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
TELEPK: 66141 PENNIE
INFORMATION FOR BQ IN NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 3;
Pred. No. 0.58;
                                                                    Score 56; DB 3;
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LiP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.9%; Score 56; DB Best Local Similarity 42.9%; Pred. No. 0.58 Matches 9; Conservative 5; Mismatches
                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 13
OTHER INFORMATION: Xaa = Aib
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                         16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                    1 PVLDEFWEKLNEXLEALKOKL 21
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PVLDEFWEKINEXLEALKOKL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: No. 6329341e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                             Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ropology: linear
                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-453-605-73
      US-09-465-719-73
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Fatent No. 6265377
Fatent No. 6265377
Fatent No. 6265377104
Fatent No. 6265377104
Fatent No. 6265377104
Fatent No. 6265377
Fatent No. 6265377
Fatent No. 6265377
Fatent No. 6265377
Fatent No. 62641, Renate
Fatent No. 62651, Renate
Fate
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.9%; Score 56; DB 3; Length 22; Best Local Similarity 42.9%; Pred. No. 0.58; Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNDER:
TILING DATE: 29-SEP-1997
ATTORNEY AGENT INFORMATION:
NAME: COTUZZ, LAURER: 30,742
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECHOME: 650-493-4935
TELEFAX: 66141 FENUE:
TELEFAX: 66141 FENUE:
TELEFAX: 66141 FENUE:
TELEFAX: 66141 FENUE:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i NAME/KEY: Other
i LOCATION: 13
i OTHER INFORMATION: Xaa = Aib
US-08-940-096-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Other LOCATION: 13 OTHER INFORMATION: Xaa = Aib
                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046166e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: No. 6265377e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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US-09-465-719-73
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                                                        APPLICANT: Dasseux, Jean-Louis
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.9%; Score 56; DB 3; Length 22; Best Local Similarity 42.9%; Pred. No. 0.58; Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DAILS:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPAX: 650-493-4935
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
Sequence 73, Application US/09453838 Patent No. 6376464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 PVTQEFWDNLEKETEGLRQEM 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 13
OTHER INFORMATION: Xaa = Aib
US-09-453-838-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: No. 6376464e
                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-940-136-73
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. COTRUL, ISABELLE

J. FLICANT: Metz, Gunther

HERAPLICANT: DECOURCY, Jean

TITLE OF INVENTION: GENE THERAPY APPROACHES TO

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

CONTRY: USP

ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Islabelle
APPLICANT: Ocrunt, Islabelle
APPLICANT: Dufourcq, Jean
APPLICANT: Sekulourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: Sekulourcq, Jean
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM ITEE DISKETCE
OMETATING SYSTEM: DOS
SOFTWARE: FRAESO VEFRION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0007-999
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
INFORMATION PRORMATICS:
SEGUENCE CHARACTERISTICS:
LENGTH: 22 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.9%; Score 56; DB 4; Best Local Similarity 42.9%; Pred. No. 0.58; Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 PVTQEFWDNLEKETEGLRQEM 36
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US-03-453-841-73
'Sequence 73, Application US/09453841
'Patent No. 6573239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 13
; OTHER INFORMATION: Xaa = Aib
US-08-940-136-73
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MOLECULE TYPE: No. 6518412e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: si
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APPLICATION NUMBER: US/09/453,833
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: Other
) LOCATION: 13
); OTHER INFORMATION: Xaa = Aib
12-09-453-833-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.99
Matches 9; Conservative
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US-09-453-833-73
is Sequence 73, Application US/09453833
is APPLICANT: Baseux, Jean-Louis
APPLICANT: Baseux, Jean-Louis
APPLICANT: Metz, Gunther
is APPLICANT: APOLICANCH
is TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
ITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
is TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
is TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
is TITLE OF INVENTION THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
is TITLE OF INVENTION DOS
is SOFTWARE: FastSEQ Version 2.0
is CURRENT APPLICATION DATA:
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27.9%; Score 56; DB 4; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 7; Indels
                                                   COUNTRY: USA

ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RECENCEPHONE: 650-493-4935
TELEPHONE: 650-493-4935
TELEPHONE: 660-493-4935
TELEPHONE: 660-493-556
TELEFA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 PVTQEFWDNLEXETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PVLDEFWEKLNEXLEALKOKL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa = Aib US-09-453-841-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: Other
     New York
CITY: Ne
STATE: N
COUNTRY:
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RESULT 11
US-09-453-826-73
Sequence 73, Application US/09453826
Fatent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Gunther
APPLICANT: Ornut, Teabelle
APPLICANT: Ornut, Teabelle
APPLICANT: Ornut, Jeabelle
APPLICANT: Datourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
COTTY: New York
COINTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%; Score 56; DB 4; Length 22; 42.9%; Pred. No. 0.58; tive 5; Mismatches 7; Indels
PRILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTIZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,999
TELECOMMUNICATION INFORMATION:
TELEPAK: 660-493-4935
TELEX. 66141 PENNIE
INFORMATION FOR SEQ. D1 NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFRATE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
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Sequence 73, Application US/09865989
Sequence 73, Application US/09865989
Patent No. 6734169
GENERAL INPORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Metz, Gunther
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                Gaps
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COUNTRY: USA
ZIP: 10036-2811

COMPUTER REDABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESGO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-MAY-2001
CLASSIFICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INDER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INDER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
SECONDATION: 550-493-5556
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acide
TYPE: amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 22; 0.58;
                                                                                                                                                                                                                       Length 22;
                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB
Pred. No. 0.58
5; Mismatches
                                                                                                                                                                                                              Query Match
27.9%; Score 56; DB
Best Local Similarity 42.9%; Pred. No. 0.58
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 73: US-09-865-989-73
                                                                                                                                                                                                                                                                                                                                          16 PVTOEFWDNLEKETEGLROEM 36
                                                                                                                                                                                                                                                                                                                                                                                1 PVLDEFWEKLNEXLEALKOKL 21
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                                                                                                                           Xaa = Aib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 258
MOLECULE TYPE: No. 6716816e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other
13
                                                            ) NAME/KEY: Other;

; LOCATION: 13

; OTHER INFORMATION:

US-09-453-840-73
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APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%; Score 56; DB 4; Length 22; 42.9%; Pred. No. 0.58; tive 5; Mismatches 7; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTENCY O'EFSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLILON
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION VUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00915
TELECOMMUNICATION INFORMATION:
TELEFAK: 650-493-5556
TELEFAK: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
TENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PVTOEFWDNLEKETEGLROEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73, Application US/09453840 Patent No. 6716816 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 13
CTHER INFORMATION: Xaa = Aib
US-09-453-826-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: No. 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9°
Matches 9; Conservative
                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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US-09-453-840-73
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Search completed: December 21, 2004, 12:15:07 Job time : 40 secs
GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: Bakul, Renate

APPLICANT: Sekul, Renate

APPLICANT: Cornut, Isabelle

APPLICANT: Gornut, Isabelle

APPLICANT: Metz, Gunther

APPLICANT: Metz, Gun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Pennie & Edmonde Lur
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: PERSESO Version 2.0
SOFTWARE: PERSESO Version 2.0
SOFTWARE: PERSESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE: 29-SEP-1997
ATTOMEN/AGENT INFORMATION:
NAME: COLUZZI, LAURA APPLICATION NUMBER: 009196-0004-999
FELENCOMMUNICATION INFORMATION:
NAME: COLUZZI, LAURA APPLICATION OF SECTION OF S
                                                  16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                 1 PVLDEFWEKLNEXLEALKOKL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 73, Application US/09453834 Patent No. 6753313
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; OTHER INFORMATION: Xaa = Aib
US-09-453-834-73
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Best Local Similarity 42.99
Matches 9, Conservative
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Sequence 8, Application US/07928930A Patent No. 5344822

US-07-928-930A-8

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Gaps
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                                                                                                                                                                                                                                                 ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,930A

FILING DATE: 19920812

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5344822man D.

REGISTRATION NUMBER: 30,946
APPLICANT: Levine, Daniel M.; Parker, Thomas S.;
APPLICANT: Rubin, Albert L.
TITLE OF INVENTION: Methods Useful in Endotoxin
TITLE OF INVENTION: Prophylaxis and Therapy
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PVTQEFWDNLEKETEGLRQEM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: ROGG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPKX: (212) 688-9200
TELEPKX: (212) 838-3864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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Matches 10; Conserva
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using
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December 21, 2004, 11:46:06 ; Search time 38 Seconds	(without alignments)	283.586 Million cell updates/sec
Run on:		

US-09-803-918A-2_COPY_156_267 556 1 OKLHELQEKLSPLGEEMRDR.....SFKVSFLSALEEYTKKLNTQ 112 score: Perfect Title:

Scoring table: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

46225 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 112

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1,1000					SUMMARIES	·
No.	Score	Match	Length	DB	αI	Description
п	67	12.1	7.1	7	I51705	stathmin - African
7	66.5	12.0	104	7	A32731	somatoliberin prec
m	64	11.5	88	~	H87560	conserved hypothet
4	62.5	11.2	109	-	IWBO	ATPase inhibitor p
ഹ	62	11.2	97	~	T46234	hypothetical prote
9	62	11.2	107	7	876457	hypothetical prote
7	61	11.0	104	7	A12730	ㅁ
80	61	11.0	108	7	A59010	antifreeze protein
σ	59.5	10.7	97	7	AB1439	small heat shock p
10	59.5	10.7	102	~	A13243	transcriptional re
11		10.7	102	~	T03423	traM protein - Agr
17		10.6	73	~	B70542	hypothetical prote
13	59	10.6	110	~	E81366	ч
14	59	10.6	111	~	T50084	hypothetical coile
15	58.5	10.5	107	Н	F69228	hypothetical prote
16		10.3	108	~	G83073	_
11	57	10.3	98	N	F64527	_
18	57	10.3	94	~	PS0349	myosin heavy chain
13	57	10.3	96	~	C98046	ы
20	57	10.3	96	~	D95179	ribosomal protein
21	57	10.3	110	~	B83481	hypothetical prote
55	56.5	10.2	91	~	I54248	apolipoprotein A-I
23	56.5	10.2	66	7	JU0038	nonhistone chromos
24	56.5	10.2	104	~	E69805	hypothetical prote
25	26	10.1	79	7	F91093	
56	56	10.1	93	~	AE1522	hypothetical prote
	26	10.1	98	~	E85747	
58	99	10.1	101	~	C83539	morphogene protein
53	55.5	10.0	97	~	AI1081	a small heat shock

intermediate filam hypothetical prote	hypothetical prote conserved hypothet	conserved hypothet conserved hypothet	transcription regu	apolipoprotein Cl	conserved hypothet	hypothetical prote	hypothetical prote	outer membrane lip	peptidyl-prolyl ci	conserved hypothet	hypothetical prote	hypothetical prote
S44095 T50611	T29123 AF1306	AF1678 AC0895	F83736	148251	B87263	H90509	T05224	A33854	AE0923	D89792	T39864	A72717
00	0 0	~ ~	N	~	N	N	~	~	~	~	N	0
98 100	109 97	97 101	109	88	106	107	67	83	93	97	112	112
10.0	10.0 9.9	0 0 0 0	9.9	8.6	ø.	9.6	9.7	9.7	9.6	9.6	9.6	9.6
55.5	55.5 55	555	55	54.5	54.5	54.5	54	54	53.5	53.5	53.5	53.5
30 31	3 3 3 3	3.4 3.5	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Grathmin - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Accession: 151705
R;Maucuer, A.; Moreau, J.; Mechali, M.; Sobel, A.
J. Biol. Chem. 268, 16420-16429, 1993
A;Title: Stathmin gene family: phylogenetic conservation and developmental regulation in A;Reference number: A47345; MUID:93346387; PMID:8344928
A;Accession: 151705
A;Accession: I51705
A;Accession: I51705
A;Genetics: Drainminary; translated from GB/EMBL/DDBJ
A;Accession: T1 cMAU>
A;Cross-references: UNIPROT:Q09005; EMBL:X71432; NID:g397171; PIDN:CAA50563.1; PID:g397
C;Genetics:
A;Cross-references: UNIPROT:Q09005; EMBL:X71432; NID:g397171; PIDN:CAA50563.1; PID:g397
C;Superfamily: stathmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.1%; Score 67; DB
Best Local Similarity 38.5%; Pred. No. 53;
Matches 20; Conservative 11; Mismatches
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# 86 35 YSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLROG 셤

Accession: A2731

NiAlternate names: growth hormone-releasing hormone
(Sipecies Rattue norwegicus (Norway rat)
(Sipecies Rattue norvegicus (Norway rat)
(Sipecies I-104 cMay)

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A,Title: Amino acid sequence of the protein inhibitor of mitochondrial adenosine triphos A,Reference number: A01336, MUID:82150878; PMID:6461003
A,Accession: A01336
A,Accession: A01336
A,Molecule type: protein
A,Residues: 26-54,'Q',56-109 cFRA>
A,Note: there are several internal duplications near the carboxyl end (residues 73-97)
C,Comment: This peptide is thought to be a regulatory component of the ATP-synthesizing C,Superfamily: ATPase inhibitor, mitochondrial
C,Superfamily: ATPase inhibitor, mitochondrian
F,1-25/Domain: transit peptide (mitochondrian) #status predicted <SIG>
F;26-109/Product: ATPase inhibitor #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Synechocyetis sp.
Cispecies: Synechocyetis sp.
Cispecies: Synechocyetis sp.
A;Variety: PCC 6803
Cibate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 376457
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.,
C, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud^NA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: T46234
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GEEMRDRARAHVDALR-----THLAPYSDELRQRLAARLEALKENGGARLAEYHAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 62.5; DB 1; Length 1; Pred. No. 1.9e+02; 13; Mismatches 36; Indels
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A;Experimental source: cultivar Columbia; BAC clone T9C5
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A,Accession: S76457
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85 IERLQKEIERHKQSIKKLKQ 104
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Best Local Similarity 21.09
Matches 17; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-97 <RIE>
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A;Cross-references: GB:M73486; NID:g204311; PIDN:AAA41220.1; PID:g204312
R;Srivastava, C.H.; Monts, B.S.; Rothrock, J.K.; Peredo, M.J.; Pescovitz, O.H.
Endocrinology 136, 1502-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-1508, 1802-
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Cipecies: Caulobacter crescentus
Cipecies: Caulobacter crescentus
Cipecies: Caulobacter crescentus
Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
Cipacession: H87560
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzaray, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: C27382, A01316
E;Accession: C27382
E;Asion: C37382
E;Asi
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A;Reaidues: 1-88 STO>
A;Cross-references: UNIPROT:Q9A5D7; GB:AE005673; NID:g13424070; PIDN:AAK24484.1; GSPDB:C
C;Genetics:
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; Pred. No. 86;
10; Mismatches
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32.9%;
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Best Local Similarity 32.5.
Best Local Similarity 32.5.
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small heat shock protein of Clostridium acetobutylicum homolog lin0049 [imported] - Lis
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C; Species: Listeria innocua
C; Species: Listeria innocua
C; Species: Listeria innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Date: 27-Nov-2001
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
O, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AB1439
A; Status: preliminary
A; Molacule type: DNA
A; Residues: 1-97 GLAA
Cross-references: UNIPROT:Q92FQ4; GB:AL592022; PIDN:CAC95282.1; PID:g16412470; GSPDB:CCGGnetics:
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Cispecies: Chen, Mood, G.E.; Chen, Mood, G.E.; Chen, M.; Wood, G.E.; Chen, M.; Mood, G.; Gillet, W.; Garatt, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
AiAuchors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ater, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A,Experimental source: strain C58 (Dupont)
                                                                                                                                               10 LSPLGEEMRDRARAHVDALRTHLAPYSDEL--RQRLAARLEALKENGGARLAEYHAKATE 67
                                                                                                                                                                                                       6 LESLGQ------YFEEMKTKLIQDMTEIIRSQDLANQAQAFVEDKKTQLQPLVAQIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::|| |:||||: : |: |: |: |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- |
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                                                                                                                                                                                                                                                                                                                                                 68 HLSTLS----EKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ 112
                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 59.5; DB 2; Length 97; 25.3%; Pred. No. 2.9e+02; cive 20; Mismatches 30; Indels ;
22.9%; Pred. No. 2.5e+02;
tive 24; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 59.5; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ---PKVTEF-ANLMDQINDQLEKTANAVEEHDQQL
Best Local Similarity 22.99
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
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Matches 24; Conserv
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A; Residues: 1-102 < KUR>
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A; Status: preliminary
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A;Gene: traM
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: lin0049
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Rocession: A12730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 «KUR»
A;Ross-references: UNIPROT:Q8UPZ0; GB:AE008688; PIDN:AAL42263.1; PID:g17739660; GSPDB:GC;Genetics:
A;Cross-references: UNIPROT:Q8UPZ0; GB:AE008688; PIDN:AAL42263.1; PID:g17739660; GSPDB:GC;Genetics:
A;Gene: Atu1254
A;Map position: circular chromosome
                                        A;Cross-references: UNIPROT:P74485; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA1858
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CjAccession: A12730
R;Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription regulator, ArsR family Atu1254 [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä;
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                                                                                                                                                                                                                                                                                                                                                                                               7 QEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLA-----ARLEALKENGGARLA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 APCQDMPRSTLSSHWRILREAG---LIRTHKQGVENISVV-----RLEDMEARFPGLLP 96
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C;Species: Myoxocephalus octodecimspinosis (longhorn sculpin)
C;Species: Myoxocephalus octodecimspinosis (longhorn sculpin)
C;Species: Myoxocephalus octodecimspinosis (longhorn sculpin)
C;Species: Oct.-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C;Accession: AS9010
R;Deng, G.; Andrews, D.W.; Laursen, R.A.
FRBS Lett. 402, 17-20, 1997
A;Reference number: AS9010; MUID:97165956; PMID:9013849
A;Recession: AS9010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-108 < LAU>A;Residues: UNIPROT:P80961
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C;Keywords: antifreeze; plasma; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                             Query Match
11.2%; Score 62; DB 2; Length 107;
Best Local Similarity 23.9%; Pred. No. 2e+02;
Matches 21; Conservative 17; Midmatches 30; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels 12;
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A; Residues: 1-107 < KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SILKF 101
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9

Length 102;

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probable membrane protein C10926 [imported] - Campylobacter jejuni (strain NCTC 11168) C; Species: Campylobacter jejuni (cjoute: 31-Mar-2000 #text_change 09-Jul-2004 C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C; Accession: E8136 R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000 A; Fitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyr A; Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-110 <PAR>
A;Cross-references: UNIPROT:Q9PP07; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7318
A;Experimental source: serotype O2, strain NCTC 11168
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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Accession: F69228
R;Smith, D. R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J. Ratteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
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    fission yeast (Schizosaccharomyces pombe)

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R;Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999
A;Reference number: Z25035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical coiled-coil protein [imported] - fission yeast (Schizosaccharon
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 38.2%; Pred. No. 3.7e+02;
Matches 21; Conservative 12; Mismatches 12; Indels 10;
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A;Introns: 12/1; 15/2; 64/3
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YGL029w
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A;Experimental source: strain 972h(-); cosmid c1556
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C,Genetics:
A,Gene: tram
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R;Cole, S.T.; Broach, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Davies, R.; Davies, R.; Davies, R.; Davies, R.; Davies, R.; Selton, S.; Skelton, S.; Squares, S.; Anthors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500; MUD: 98295987; PMID: 9634230
A; Reference number: A70500; MUD: 98295987; PMID: 9634230
A; Reference number: A70500; MUD: 98295987; PMID: 9634230
A; Residues: Dreliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-73 <COL.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tram protein - Agrobacterium tumefaciens plasmid pTiC58
C;Species: Agrobacterium tumefaciens
C;Species: To Agrobacterium tumefaciens
R;Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwang, I.; Kim, H.; Farrand, S.K.
B;Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwang, I.; Kim, H.; Farrand, S.K.
B;Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwang, I.; Kim, H.; Farrand, S.K.
B;Piper, R.M.; Farrand, M.; Farrand, S.K.
B;Piper, Burbar, Farrand, M.; Farrand, S.K.
B;Piper, B.M.; Farrand, M.; Farrand, S.K.
B;Molecule type: DMA
A;Residues: II102 <PIP>
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                                                                                                                9 KLSPL----GEEMRDRARAHVDALRTH--LAPYSDELRORLAARLEALKENGGAR---- 57
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 09-Ju1-2004
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                                         Indels
                                     27;
ilarity 32.1%; Pred. No. 3.1e+02;
Conservative 11; Mismatches 27
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| EASIEMHAQMSA-VSTL 89
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A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
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A/Fesiduse: 1-107 < MTH>
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A/Fesiduse: 1-107 < MTH>
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Query Match 10.5%; Score 58.5; DB 1; Length 107; Best Local Similarity 27.8%; Pred. No. 3.9e+02; Matches 27; Conservative 15; Mismatches 34; Indels 21; Gaps

3 LHELQEKLSPIGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYH 62 

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63 AKATEHLSTLSEKAKPALEDLR---QGLLPVLESFKV 96
:| :| || || :| || || 67 ERARKEAIEISGKAKREVETMKSAAMGKVPEAASIIV 103

Search completed: December 21, 2004, 11:56:35 Job time : 41 secs

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                                                                                  December 21, 2004, 11:47:05; Search time 186 Seconds
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AAS81257
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Listing first 45 summaries
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MEDLINE=99216322; PubMed=10198255;
Hamidi Asl K., Lispnikas J.J., Nakamura M., Parker F., Benson M.D.;
Hamidi Asl K., Lispnikas J.J., Nakamura M., Parker F., Benson M.D.;
Hamidi Asl K., Lispnikas J.J., Variant, Arg173Pro, associated with
cardiac and cutaneous amyloidosis.";
La Biochem. Blophys Res. Commun. 227:584-588 (1999).
Biochem. Blophys R. Res. Commun. 277:584-588 (1999).
BMBL; AF149663; AD34664.1;
CO; GO:0008289; Filipid binding; IEA.
CO; GO:0008289; Filipid binding; IEA.
CO; GO:0008869; Pilipid transport; IEA.
CO; GO:0008889; Pilipid transport; IEA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 2e-19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TDB0,
Q8TDB0;
01-JUN-2002 (TrENBLrel. 21, Created)
01-JUN-2002 (TrENBLrel. 21, Last sequence update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
Apolioporotein A-1 A175P variant (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                        Q81Q79
Q8R814
Q9QJL5
APC1_TUPGL
Q92FQ4
TRAM_AGRT5
Q9R6E6
Q711L8
CAC86373
Q8P6R7
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Q8KKD9
AAS93839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.8%;
larity 98.5%;
Conservative
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Homo sapiens (Human)
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APE_SAISC
028995;
                                                                                                                                       Name=APOE;
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SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams T.D., Gensberg K., Minchin S.D., Chipman J.K.,
"A DNA expression array to detect toxic stress response in European flounder (Platichthys flesus).",
Aquat. Toxicol. 65:141-157(2003).
EMBL, AJ310423; CAC27154-1;
GO, GO:0002556; Cextracellular; IEA.
GO; GO:000289; F:lipid binding; IEA.
GO; GO:0006889; P:lipid transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Platichthys fleeus (European flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metozoa; Chordata; Craniata; Vertebrata; Neofeleosteni;
Acainohomerypii; Acanthoperygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Platichthys.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                          1 HVDALRTHLAPYSDELRQRLPARLEALKENGGARLAEYHAKATEHLSTLS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 102;
                                                                                                                                                                                                                                                                            24 HVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLS
                                                                                                                                                                                                                                Length 50;
                                                                                                                                                                                                                               Query Match
44.2%; Score 246; DB 2; Length 50
Best Local Similarity 98.0%; Pred. No. 5.9e-13;
Matches 49; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                        Booth D., Bybee A., Pepys M., Hawkins P.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF485255; AAL92035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1 1 1 1 1 1 102 AA; 11248 MW; 8F0EB2150625EDFA CRC64;
                                                                                                                                                                                   1 1
50 50
50 AA; 5607 MW; A65219AE9E965732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein AI (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%; Score 109.5; DB 2; 27.6%; Pred. No. 0.16; ive 20; Mismatches 40;
                                                                                                  GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008289; F:lipid binding; IEA.
GO; GO:0008689; P:lipid transport; IEA.
InterPro; IPR000074; Apolipoprotein metabolism; IEA.
PEam; PF01442; Apolipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0042157; P:lipoprotein metabolism; IEA.
InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo A E C3.
Pfam; PF01442; Apolipoprotein; I.
                                                                                                                                                                                                                                                                                                                                                           102 AA
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MEDLINE-22827201; PubMed=12946615;
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Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                           SEQUENCE FROM N.A.
                                                                                         HSSP; P02647; 1AV1
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           Mammalia; Euther
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8260;
                                                                                                                                                                         Lipoprotein.
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NON TER
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oŧ
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                     Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDL receptor binding (Potential).
Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipoprotein.
Pfam; PF01442; Apolipoprotein; I.
Chylomicron; Glycoprotein, HDL; Heparin-binding; Lipid transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA; 12328 MW; FF88CED47BD18F7C CRC64;
                             9
62 AQAVKPEDLTALKEKISPMAEBVKAKVTEMFEAIAATF
                                                                                                                                                                                                  (Rel. 37, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                      Ž
                                                                                                                                                                                                                                           Apolipoprotein E (Apo-E) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LASHLRKLRKRLLRDVDDLQK 106
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                                                                                                                                                                              (Rel. 37, Created)
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                                                                                                                                      STANDARD;
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96
>107
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54
76
98
>107
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P02649;
                                                                                                                                                                              15-DEC-1998
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62 -HAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSF 98

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3 LHELQEKLSPLGEENRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYH 62
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KREDLINE=21886394; PubMed=11889109;
KREDLINE=21886394; PubMed=11889109;
KREDLINE=21886394; PubMed=11889109;
KREDLINE=21886394; PubMed=11889109;
KREDLINE=21886394; PubMed=11889109;
KREDLINE=21886394; PubMed=11889109;
KREDLINE=21886394; PubMed=1, Lykidis A., Lykidis A., Gardner W., Grechkin G., Zhu L., Lykidis A., Gardner W., Grechkin G., Zhu L., Lykidis A., Wallus T., Pusch G., Goltsman E., Bernal A., Larsen N., D'Scolza N., Overbeek R., Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATC 25586.";
In Cenome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATC 25586.";
I. J. Bacteriol. 184:2005-2018(2002).
KREL; AEO10521; AAL94275.1; -.
KREL; AEO10521; AAL94275.1; -.
KREPPRO; IPR004238; LEA.;
KREM: PF02997; LEA.4; 1.
KOMPLete proteome; Hypothetical protein.
KREM: SEQUENCE 96 AA; 10403 MW; 7C830AE39E66E885 CRC64;
                                                                                                                                                                                             Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.; Submitted (JAN-2003) to the ShBL/GenBank/DDBJ databases - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                      Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 96; 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Indels
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                                                                                                                                                                                                                                                                                         preliminary data.

EMBL, AABFO1000220; EAA23153.1; -.
Interpro; IPR004238; LEA.
Pfam; PR05987; LEA 4; 1.
Hypothetical protein.
SEQUENCE 96 AA; 10436 MW; 7568787BAFE86350 CRC64;
            01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                           14.2%; Scor.
23.2%; Pred. No. 4.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical cytosolic protein.
OrderedLocusNames=FN0062;
                                                           Hypothetical cytosolic protein.
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 23.5*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.2*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                       NCBI_TaxID=209882;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                  STRAIN=ATCC 49256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusobacterium
                                                                          Name=FNV0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8RH51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 QVTQELTTI.MDETWKELKAYKSELEEQLSPVAEETRARLSKELQAAQARI.GADMEDVRSR 63
                                                                                                                                                                                                                                         Heparin-binding (By similarity).
8 X 22 AA approximate tandem repeats.
                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000074; Apolipoprotein.
InterPro; IPR009074; Apolipo_A E_C3.
InterPro; IPR004974; Apolipo_A E_C3.
Emi; PPG10442; Apolipoprotein; 1.
Chylomicron; Glycoprotein; HDL; Heparin-binding; Lipid transport;
Plasma; Repeat; VLDL.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDL receptor binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                   remnant) of hepatic tissues.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Secreted in plasma.
-!- SIMILARITY: Belongs to the apolipoprotein Al/A4/E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 93; DB 1; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12382 MW; E1D38C32F5AACB23 CRC64;
                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
Apolipoprotein E (Apo-E) (Fragment).
                           107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                     Macaca mulatta (Rhesus macaque)
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                            STANDARD;
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Les 23; Conserv
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                           APE MACMU
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MEDLINE-22862880; PubMed-14500782;

MEDLINE-22862880; PubMed-14500782;

MEDLINE-22862880; PubMed-14500782;

MEDLINE-22862880; PubMed-14500782;

MEDLINE-22862880; PubMed-14500782;

MATCONIO R.V., Almeida E.C., Hungria M., Guimaraes C.T.,

Ascolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,

Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Ferrara D.M.,

Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Ferrara D.M.,

Cartapaglia D., Grisard E.C., Fraitas I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,

Mactapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,

Macimento S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,

Mascimento F.F., Nicolas M.F., Oliveira J.G., Pereira J.C.,

Partan M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,

Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,

Santos B.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,

Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R.N., Souza K.R.L.,

Santos B.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,

Silva A., Wassen R.P., Santos R.B., Meishen R., Sancos C.M.A., Soares C.M.A., Soares R.B.A., Santos R.B., Warberden R., Stingen R., Stingen
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61
                                             10 KAEELVGAVTDKAKELKDETVAKAEELKDKTVEKAEELKNKVVDKAKELKEGAEGKASEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LABLIBQLEPLTRELLEAANLRDRPRFSSLYGRSEAHVQQLLKTLEQBGRDQLSDBQREA
KLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEY
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Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
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EMBL, AE016923; AAQ61536.1; -.
Complete proteome; Hypothetical protein.
continuore 110 AA; 12757 MW; 6B6CC3929C615493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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L-HRVLIVREETQRQLANWAGQVKDELRTLSKSSK 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA.
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                                                                                                                                                              HAKATEHLSTLSEKAKPALEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromobacterium violaceum.
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es 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                              RESULT
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RESULT 9

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Inomata T., Hanawa H., Miyanishi T., Yajima E., Nakayama S., Maita T.,
Kodama M., Izumi T., Shibata A., Abo T.;
"Localization of porcine cardiac myosin epitopes that induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 OKLHELQEKLSPLGEEMRDR--ARAHVDALRTHLAPYSDELRQRLAARLEALKENGGA 56
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                                                                                                                                                      Gillichthys seta (Shortjaw mudsucker).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidei;
Gobiidae; Gillichthys.
                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver;

X MEDLINE-2117151; PubMed=11172064;

AGRACEY A.Y., Towned G.N.;

Gracey A.Y., Somero G.N.;

Hypoxia-induced gene expression profiling in the euryoxic fish Gillichthys mirabils.";

Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).

R MBL; AFZ66178; ARG13298 1.;

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005899; F:lipid binding; IEA.

GO; GO:0006899; P:lipid binding; IEA.

GO; GO:0006899; P:lipid binding; IEA.

R GO; GO:000674; Apolipoprotein.

R InterPro; IPR000074; Apolipoprotein.

R Pfam; PF01442; Apolipoprotein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 KLSPLGEEMRDRARAHVDALRTHLAPYSDELRORLAARLEAL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                experimental autoimmune myocarditis.";
Circ. Res. 76:726-733(1995).
Interepro; IPR002928; Myosin tail.
Pfam; PF0175; Myosin tail.
SEQUENCE 96 AA; 11137 MW; 69943C386226BEEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
66
7637 MW; 0B5B673FA8C91B7D CRC64;
                                                                        01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Apolipoprotein A-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%; Score 77; DB 2; 33.3%; Pred. No. 47; stive 13; Mismatches 1
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37.9%; Pred. No. 75;
tive 11; Mismatches
                                                     Created)
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Sus scrofa (Pig).
                                                     (TrEMBLrel. 16,
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nes 22; Conservative
PRELIMINARY;
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66 AA;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                               Gobiidae, Gillicht
NCBI_TaxID=79683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoprotein.
NON TER
                                                     01-MAR-2001
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                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=PEST;
                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                               Lipoprotein.
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                     029258
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RESULT 13
Q29258
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                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  3 LHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAE
                                                                                                            OrdefedLocusNames=TTC0913;
Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                       Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus
                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                      13.0%; Score 72.5; DB 2; Length 104; ilarity 37.9%; Pred. No. 1.7e+02; Conservative 8; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2004 (TrEMBLrel. 27, Created)
14-ARR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
V-type ATPase subunit.
TTC0913.
Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.0%; Score 72.5; DB 2; Length 104; 37.9%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Biotechnol. 22:547-553(2004).
EMBL; AE017304; AAS81257.1; -.
SEQUENCE 104 AA; 11672 MW; A01FBCE249900B1F CRC64;
                                                                                                                                                                                                                                                                                                                 104 AA; 11672 MW; A01FBCE249900B1F CRC64;
                                                                             Last sequence update)
Last annotation update)
                                             104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AA
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                                                                   Created)
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EMBL; AE017304; AAS81257.1; -.
                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                           PRELIMINARY;
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                                                                                                     V-type ATPase subunit
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Best Local Similarity
22; Conserve
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Best Local Similarity
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PubMed=15064768;
                                                                                                                                                           NCBI_TaxID=262724;
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SEQUENCE 104 AA
                                                                                                                                                                                               PubMed=15064768;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Small intestine;

BDLINES2637607, PubMed=8672129;
Winterce A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine CDNA
                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 70; DB 2; Length 102
31.2%; Pred. No. 2.7e+02;
iive 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AA; 11534 MW; 123EAEEA134FBC8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 AA; 9772 MW; 769097995041FB44 CRC64;
                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         = = :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mamm. Genome 7:509-517(1996).

EMBL, F14546; CAA23119.1; -.

GO, GO:0005576; C:extracellular; IEA.

GO; GO:0006889; F:lipid binding; IEA.

GO; GO:0008869; P:lipid transport; IEA.

GO; GO:0004287; P:lipid transport; IEA.

InterPro; IPR00074; Apolipoprotein.

InterPro; IPR009074; Apolipo_A_E_G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgCP8687 (Fragment).
Name=agCG49971; ORFNames=ENSANGG00000007463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AA
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EMBL; AAAB01008980; EAA14425.1;
                                                                                                                                                 Apolipoprotein A-IV (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01442; Apolipoprotein;
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les 15; Conservative
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PRELIMINARY;
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Db 16 NDLNVRINSRCEAVQGEVDAFVDEYVAALEEHRCTLSER----IGNIREAKGMKIIMAQKL 71

RESULT 15

QGLD50

10 QGLD50

10 QGLD50

11 QGLD50

12 QGLD50

13 QGLD50

14 QGLD50

15 QGLD50

15 QGLD50

16 GGLD50

17 GG-JUL-2004 (TREMBLrel. 27, Created)

18 QGLD50

19 GG-JUL-2004 (TREMBLrel. 27, Last sequence update)

19 GG-JUL-2004 (TREMBLrel. 27, Last sequence update)

10 GG Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Mus.

10 GG Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Mus.

11 Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Mus.

12 Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Mus.

13 GGLG100

14 Machine Sciurognathi, Musidae, Mus.

15 Merrill JT., Rivkins E., Shen C., Lahita R.G.;

16 Merrill JT., Rivkins E., Shen C., Lahita R.G.;

17 Merrill JT., Rivkins E., Shen C., Lahita R.G.;

18 Merrill JT., Rivkins E., Shen C., Lahita R.G.;

18 Merrill JT., Rivkins Rheum. 38:1655-1659(1955).

19 Rest. Local Similarity JT.M;

12 Merrill JT. Score G7.5; DB 2; Length 79;

12 Merchan Matches 20; Conservative 15; Mismatches 24; Indels 33; Gaps 1;

19 Merrill JT. Matches 20; Conservative 15; Mismatches 24; Indels 33; Gaps 1;
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Search completed: December 21, 2004, 11:59:49 Job time : 191 secs

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63 AKATEHLSTLSEKAKPALEDLRQGLLPVLESF 94

------ESARQKLQELQGRLSPVAEEF

59

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ADC29637
ADP87430
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                                                                                                                                                                                                                                                                                                                                                                         Human ApoA-I protein fragment.
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UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2002; 2002WO-CA001615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-2001; 2001US-0335075P.
                      8667727777888
 WPI; 2003-449258/42.
 WO2003035691-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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ABR44037;
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Human Apo
Human Apo
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Baboon Ap
Rabbit Ap
Antioxida
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Antioxida
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Baboon ap
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Rhesus ma
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Antioxida
Antioxida
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Monkey ap
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                                                                         December 21, 2004, 11:55:03 ; Search time 152 Seconds (without alignments) 264.327 Million cell updates/sec
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Compugen Ltd.
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1 QYLHELQEKLSPLGEEMRDR.......
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Copyright (c) 1993 - 2004
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Maximum Match 100%
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ADC29656
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ADC29639
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ADP87422
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Gapop 10.0 , Gapext 0.5
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geneseqp2003a8:*
geneseqp2003bs:*
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geneseqp1980s:*
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                                                    - protein search, using
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length: 112
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Match
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Perfect score:..
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157:1
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Result No.

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Human Apo
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Chimpanze
Amplified
Mouse apo
Mouse apo
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Adc29627
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43.9%; Score 244; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 49; Conservative 0; Mismatches 0; Indels
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ADC29627
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ABR44039

RESULT

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The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polymuclochide is useful for preparing a composition for treating cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly conserved except in pig (ABR44042)
                                                                                                                                                                                                                                              useful for preparing a composition for
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43.9%; Score 244; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 49; Conservative 0; Mismatches 0;
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treating cardiovascular disorder
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treating cardiovascular disorder
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                                                                                                                               (XENO-) XENON GENETICS INC. (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XENO-) XENON GENETICS INC. (UYBR-) UNIV BRITISH COLUMBIA.
                                                               25-OCT-2002; 2002WO-CA001615.
                                                                                              26-OCT-2001; 2001US-0335075P.
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WO2003035691-A1
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                 DALKTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSE 49
DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSE 74
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Local Similarity 100.0%; Pred. No. 1.9e-17; les 49; Conservative 0; Mismatches 0;
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                                                                                                               ABR44039 standard; peptide; 49
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UNIV BRITISH COLUMBIA.
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                                                                                                                                                                                (first entry)
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56
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Best Loc Matches

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ABR44038

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Gaps

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New cysteine-containing peptides, having antioxidant properties, useful for diagnosing and treating cardiovascular disease, ischemia, bone disease and other inflammatory related diseases.
                                                                                                                                 cardiovascular disease; ischaemia; bone disease; related disease; human.
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 ADC29656 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                      08-MAY-2002; 2002US-00142238
                                                                                                                                                                                                                                                                                                                                     09-MAY-2001; 2001US-0289944P
                                                                  (first entry)
                                                                                                   Antioxidant peptide #31
                                                                                                                                                                                                                                                                                                                                                                      (BIEL/) BIELICKI J K.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-786946/74.
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                   antioxidant;
                                                                                                                                                   inflammatory
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                                                                  18-DEC-2003
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                                                                                                                                                                                      Synthetic.
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                                   ADC29656;
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The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polymuclocide is useful for preparing a composition for treating cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly conserved except in pig (ABR44042)
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                                                                                                                                                   Length 49;
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                                                                                                                                                 Score 240; DB 6;
Pred. No. 4.8e-17;
1; Mismatches 0;
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Pred. No. 1.5e-11;
4; Mismatches 7;
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UNIV BRITISH COLUMBIA
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98.0%;
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Best Local Similarity 77.6%;
Matches 38; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-449258/42.
                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003035691-A1.
                                                                                                                   Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brownlie AJ,
                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                        ABR44041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
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(UYBR-)
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                                                                                                                                                                                                                                                                                                      RESULT
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The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
                                                                                                                                                                             Gaps
                                                                                                                                                                             ö
                                                                                                                                      ch 29.0%; Score 161; DB 7; Length 33; 1 Similarity 100.0%; Pred. No. 3.3e-09; 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; pig; cardiovascular disorder.
                                                                                                                                                                                                               78 PALEDLROGLLPVLESFKVSFLSALEEYTKKLN 110
                                                                                                                                                                                                                                              33
                                                                                                                                                                                                                                   PALEDLRQGLLPVLESFKVSFLSALEEYTKKLN
                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                   ABR44042 standard; peptide; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2002; 2002WO-CA001615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2001; 2001US-0335075P
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig ApoA-I protein fragment
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RESULT 6 ADC29656

Length 33;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR44043 standard; peptide; 47 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 4; 52pp; English
                                                                                                                                                                                                                     Chicken ApoA-I protein fragment.
                                                                                                                                                  ABR44044 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Apoliprotein A-1 mutation,
                                                                                                                                                                                                                                                                                                                                                                                               (XENO-) XENON GENETICS INC. (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                  25-OCT-2002; 2002WO-CA001615.
                    27.5%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2001; 2001US-0335075P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.2%;
53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat ApoA-I protein fragment
                                                                                                                                                                                               (first entry)
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Dube M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-449258/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                Local Similarity
                                                                                                                                                                                                                                                                                                     WO2003035691-A1
Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Brownlie AJ,
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                                                                                                                                                                                                                                                                                                                            01-MAY-2003.
Sequence 33
                                                                                                                                                                                               04-AUG-2003
                                           32;
                                                                                                                                                                                                                                                                              Gallus sp.
                                                                                                                                                                          ABR44044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR44043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                       Query Match
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ABR44043
                                            Matches
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                                                                                                                          RESULT 9
ABR44044
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                                                                                                                                                The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polymuclostide is useful for preparing a composition for treating cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly conserved except in pig (ABR44042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an antioxidant peptide. The methods and compositions of the present invention are useful for diagnosing and treating cardiovascular disease, ischaemia, bone disease and other inflammatory related diseases. The present sequence represents the amino acid sequence of a peptide with antioxidant activity.
                                                                                       New Apoliprotein A-1 mutation, useful for preparing a composition for treating cardiovascular disorder.
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cysteine-containing peptides, having antioxidant properties, us for diagnosing and treating cardiovascular disease, ischemia, bone disease and other inflammatory related diseases.
                                                                                                                                                                                                                                                                                ı,
                                                                                                                                                                                                                                                                                                                  antioxidant; cardiovascular disease; ischaemia; bone disease; inflammatory related disease; human.
                                                                                                                                                                                                                                                                                                     26 DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSE
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                       Score 157.5; DB (
Pred. No. 1.2e-08
                                            Hayden MR;
                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; SEQ ID NO 30; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    standard; peptide; 33 AA.
                                            Samuels M,
                                                                                                                           Disclosure; Fig 4; 52pp; English
         (XENO-) XENON GENETICS INC. (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                       28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2002; 2002US-00142238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2001; 2001US-0289944P.
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.4'
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antioxidant peptide #30
                                            Dube M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIEL/) BIELICKI J K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-786946/74.
                                                                 WPI; 2003-449258/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003087819-A1.
                                                                                                                                                                                                                                 Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                            Brownlie AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bielicki JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                             ADC29655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polynuciocitéd is useful for preparing a composition for treating cardiovascular disorder. Sequences ABR44037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly conserved except in pig (ABR44042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; chicken; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 129; DB 6; Length 49;
Pred. No. 1e-05;
9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSE
Score 153; DB 7;
Pred. No. 2.2e-08;
                                                                                                     78 PALEDLRQGLLPVLESFKVSFLSALEEYTKKLN 110
                                                                                                                                     1 PALEDLRQGLLPVLESFCVSFLSALEEYTKKLN 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayden MR;
                                                  0; Mismatches
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and

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The invention relates to a browsable database system for use with biological information, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recogniser and an output. The invention also provides a method of operation for use with a browsable biological database system. The browsable database system and methods are useful in analysing protein sequences, classifying gene products, predicting biological role for pathway building, enhancing interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is human apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                  Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELTQQLNALFQDKLGEVNTYAGDLQKKLVPFATELHERLAKDSEKLKEEIGKELEELRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 85;
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 111; DB 8; 32.5%; Pred. No. 0.0014; iive 16; Mismatches 4
                                                                                                                                               Disclosure; SEQ ID NO 49; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ATEHLSTLSEKAKPALEDLROGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLPHANEVSQKIGDNLRELQQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA008726 standard; protein; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                 WPI; 2004-480967/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200164835-A2
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                                                                                                              output
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a mutation of the apolipoprotein A-I (ApoA-I) comprising a leucine to proline variant in position 178. The mutant ApoA-I polynucleotide is useful for preparing a composition for treating carditovascular disorder. Sequences ABRA4037-44 represent ApoA-I fragments from various species where the leucine at position 178 is highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                                                                                                                                                  New Apoliprotein A-1 mutation, useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4i H, Diemer K, Guo N;
Rabkin S, Vandergriff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 DALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKATEHLSTLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.3%; Score 113; DB 6; Length 47;
49.0%; Pred. No. 0.00041;
tive 7; Mismatches 16; Indels
         Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; rat; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human apolipoprotein A (APO-A) precursor protein.
                                                                                                                                                                                                                                                                                                              Hayden MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campbell MJ,
Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved except in pig (ABR44042)
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                                                                                                                                                                                                                                                                                                              Samuels M,
                                                                                                                                                                                                                                                                                                                                                                                                       treating cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 4; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP87442 standard; protein; 85
                                                                                                                                                                                                                                                  (XENO-) XENON GENETICS INC. (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                          25-OCT-2002; 2002WO-CA001615
                                                                                                                                                                                                               26-OCT-2001; 2001US-0335075P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-2002; 2002US-0431879P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kejariwal A,
Lazareva B,
                                                                                                                                                                                                                                                                                                            Dube M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                               WPI; 2003-449258/42.
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nes 24; Conserv
                                                                                                  WO2003035691-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47 AA;
                                                                                                                                                                                                                                                                                                          Brownlie AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Doremieux O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2004
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                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP87442;
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Matches
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ID ADP8
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09-SEP-2004
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                                                                                                                                             Sequence 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa.
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                                                                         the encoded proteins (AAO000010-AAO13910) that exhibit activity elating cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymorlectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. steem cell growth factor activity, hamalopolesis regulating activity, issue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                          invention relates to human polynucleotides (AAI79941-AAI93841) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer,
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Rabkin S, Vandergriff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                 directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Claim 20; SEQ ID NO 22618; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.0%; Score 100; DB 4; Length 38; 87.0%; Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkey apolipoprotein A (APO-A) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Muruganujan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 VLESFKVSFLSALEEYTKKLNTQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-2003; 2003WO-US038935.
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Lazareva B,
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Browsable database system, for e.g. analyzing protein sequences, and predicting a biological role, comprises a datastore, an ontology of categories of biological functions, an input receptive, a recognizer, and
interpretation of expression information, providing protein function and in facilitating comparative genomic analysis. The present sequence is monkey apolipoprotein A (APO-A) IV precursor protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                                                                                                                                                                                 2 ELTQQLNALFQDKLGEVNTYAGDLQKKLVPPATELHERLAKDSEKLKEEIRKELEEVRAR
                                                                                                                                                                                                                            5 ELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAK
                                                                                                                                                                                      Gaps
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1 S, Vandergriff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a browsable database system for use with
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                                                                                                                                         Query Match 18.0%; Score 100; DB 8; Length 85; Best Local Similarity 30.1%; Pred. No. 0.018; Matches 25; Conservative 17; Mismatches 41; Indels
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Rabkin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pig apolipoprotein A (APO-A) IV precursor protein.
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Muruganujan A,
                                                                                                                                                                                                                                                                                                        65 ATEHLSTLSEKAKPALEDLRQGL 87
                                                                                                                                                                                                                                                                                                                                                62 LLPHANEVSOKIGENVRELOORL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP87439 standard; protein; 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-2003; 2003WO-US038935.
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Ladunga I, Lazareva B,
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                                                                     5 BLQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAK 64
                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                Browsable database system; ontology; protein analysis;
gene product classification; genomic analysis; apolipoprotein A; APO-A;
                                                                                           2 ELTQQLNTLFQDKLGEVNTYTEDLQKKLVPFATELHERLTKDSEKLKEEIRRELEELRAR
                                     Gaps
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Rabkin S, Vandergriff J;
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Query Match 17.8%; Score 99; DB 8; Length 85; Best Local Similarity 28.9%; Pred. No. 0.023; Matches 24; Conservative 18; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Baboon apolipoprotein A (APO-A) IV precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 47; 113pp; English.
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Muruganujan A,
                                                                                                                                                                62 LLPHATEVSQKIGDNVRELQQRL 84
                                                                                                                                            65 ATEHLSTLSEKAKPALEDLROGL 87
                                                                                                                                                                                                                                                                      ADP87440 standard; protein; 85 AA.
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Best Local Similarity
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**ELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAK** 

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Qy 65 ATEHLSTLSEKAKPALEDLRQGL 87 | : : | : | | Db 62 LLPHANEVSQKIGENVRELQQRL 84
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Search completed: December 21, 2004, 12:02:25 Job time : 154 secs

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715.670 Million cell updates/sec
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Sequence
Sequence
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556
1 QKLHELQEKLSPLGEEMRDR.....SFKVSFLSALEEYTKKLNTQ
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| Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                              December 21, 2004, 11:10:59; Search time 56 Seconds (without alignments)
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-465-789A-58
US-10-465-789A-58
US-10-465-789A-54
US-10-465-789A-55
US-10-465-789A-56
US-10-142-238A-10
US-10-142-238A-17
US-10-142-238A-17
US-10-142-238A-17
US-10-142-238A-17
US-10-142-238A-14
US-10-142-238A-14
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                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB seq length: 112
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No.
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sequence 21, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 20, Appli
Sequence 23, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 29, Appli
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Sequence 21, Appli
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Sequence 3, Appli
Sequence 301777,
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Sequence 4, Appli
Sequence 4, Appli
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Sequence
     US-10-142-238A-15
US-10-142-238A-26
US-10-142-238A-29
US-10-142-238A-24
US-10-142-238A-24
US-10-142-238A-24
US-10-142-238A-6
US-10-142-238A-6
US-10-142-238A-16
US-10-142-238A-16
US-10-142-238A-16
US-10-142-238A-18
US-10-142-238A-29
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US-10-142-115-301777
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US-09-864-761-39472
US-10-674-755-4
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US-10-142-2384-31

Sequence 31, Application US/10142238A

Publication No. US20030087819A1

Sequence 31, Application US/10142238A

Publication No. US20030087819A1

SERNEAL INFORMATION:

APPLICANT: Bitlicki, John K.

TITLE OF INVENTION:

CURRENT PELICATION NUMBER: US/10/142,238A

CURRENT PELICATION NUMBER: US 60/289,944

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 84

SEQ ID NO 3.1

SEQ ID NO 3.1
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                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION; (1)...(33)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-31
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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NAME/KEY: PEPTIDE
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Best Local &
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RESULT 2 US-10-142-238A-30 ; Sequence 30, Application US/10142238A

Sequence Sequence Sequence

Sequence

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APPLICANT: SAPBURT, Stephner, Sapplart, Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Civjan, Natanya R
APPLICANT: Yelena V. Grinkova
APPLICANT: Ilia G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REPRENCE: 87-00A
CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT FILING DATE: 2003-66-18
FRIOR APPLICATION NUMBER: 09/990,087
FRIOR APPLICATION NUMBER: 60/252,233
FRIOR PELLOR DATE: 2000-11-20
NUMBER: OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: artificial sequence of Helix US-10-465-789A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 22; Conservative
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                 GENERAL INPORMATION:
APPLICANT: Bielicki, John K.
TITLE OF INVENTION:
CURRENT APPLICATION OWNER: US/10/142,238A
CURRENT PILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR PILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
ENGIN: BILING SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
LENGTH: 33
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US-10-465-789A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.5%; Score 153; DB 14; Best Local Similarity 97.0%; Pred. No. 8.3e-09; Matches 32; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sligar, Stephen G
APPLICANT: Sligar, Stephen G
APPLICANT: Schult, Timothy H
APPLICANT: Schult, Marchy A
APPLICANT: Schult, Matany A
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Tila G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
CURRENT FILING DATE: 2003-06-18
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(33)
COTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 PVLESFKVSFLSALEEYTKKLNTQ 112
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                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: ARTIFICIAL SEQUENCE FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
Publication No. US20030087819A1
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE
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Gaps

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Indels

Length 22;

20.3%; Score 113; DB 15; 100.0%; Pred. No. 7.4e-05; cive 0; Mismatches 0;

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19.8%; Score 110; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: artificial sequence of Helix 7
US-10-465-789A-55
Sequence 55, Application US/10465789A

Publication No. US20040053384A1

GENERAL INFORMATION:
APPLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy H
APPLICANT: Schuler, Mary A
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: 11a G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
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RESULT 6 US-10-465-789A-56

RESULT 4
US-10-465-789A-54
IS-10-465-789A-54
; Sequence 54, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:

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APPLICATION AND APPLICATION OF THE STATE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES FILE REFERENCE: 1B-1705
FILE REFERENCE: 1B-1705
CURRENT APPLICATION NUMBER: US 60/289,944
PRIOR PILLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
LENGTH: 18
                  APPLICANT: Bielicki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REFERENCE: 1B-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 18
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Publication No. US20030087819A1
GENERAL INFORMATION:
APPLICANT: Bielicki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REPRESENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142, 238A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289, 944
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Pred. No. 0.015;
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; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-13
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COTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-17
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; Publication No. US20030087819A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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US-10-142-238A-17
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US-10-142-238A-9
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Publication No. US2003087819A1
GENERAL INFORMATION:
APPLICANT: Bielicki, John K.
APPLICANT: Bielicki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REFERENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT APPLICATION NUMBER: US 60/289,944
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 18
LENGTH: 18
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19.4%; Score 108; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: artificial sequence of Helix 8 US-10-465-789A-56
                                                           APPLICANT: Sligar, Stephen G
APPLICANT: Sligar, Stephen G
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Schuler, Mary A
APPLICANT: Civian, Natanya R
APPLICANT: Yelena V. Grinkova
APPLICANT: Yelena V. Grinkova
APPLICANT: Tila G. Denisov
TILLE OF INVENTION: Membrane Scaffold Proteins
TILLE OF INVENTION: Membrane Scaffold Proteins
TILLE OF ILLING DATE: 2003-06-18
CURRENT FILING DATE: 2003-06-18
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ. ID NOS: 89
SOFTWARE: Patentin version 3.1
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; OTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-10
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US-10-142-238A-13
; Sequence 13, Application US/10142238A
; Publication No. US20030087819A1
Application US/10465789A
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                    Publication No. US20040053384A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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LENGTH: 22
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RESULT 13
US-10-142-238A-12
i Sequence 12, Application US/10142238A
j Sequence 12, Application US/10142238A
j Publication No. US20030087819A1
j GENERAL INFORMATION:
j APPLICANT: Bielicki, John K.
j TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
j FILE REFERENCE: 18-1705
j CURRENT APPLICATION NUMBER: US/10/142,238A
j PRIOR PILING DATE: 2002-08-19
j PRIOR FILING DATE: 2001-05-09
j NUMBER OF SEQ ID NOS: 84
j SEQ ID NO 12
j SEQ ID NO 12
j ENGCTH: 18
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Publication No. US20030087819A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REPRENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
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                                                                                                                                              Query Match 15.5%; Score 86; DB 14; Length 18; Best Local Similarity 94.4%; Pred. No. 0.038; Matches 17; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.048;
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     ; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)..(18); OTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-12
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                                                                                                                                                                                                                                                                                             1 GEEMRDRACAHVDALRTH 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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LENGTH: 18
TYPE: PRT
ORGANISM: ARTIPICIAL SEQUENCE
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Sequence 14, Application US/10142238A

Publication No. US20030087819A1

Sequence 14, Application US/10142238A

Publication No. US20030087819A1

APPLICANT: Bielicki, John K.

TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES

FILE REPERENCE: 1B-1705

CURRENT APPLICATION NUMBER: US/10/142,238A

PRIOR APPLICATION NUMBER: US 60/289,944

PRIOR PILING DATE: 2001-08-19

NUMBER OF SEQ ID NOS: 84

SOFTWARE Patentin Version 3.1

LENGTH: 18
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Publication No. US20030087819A1
GENERAL INFORMATION
APPLICANT: Bielicki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES FILE REPERENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT FILING DATE: 2002-08-19
PRIOR PLICATION NUMBER: US 60/289,944
PRIOR PLICATION NUMBER: 3001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                      DB 14; Length 18;
                                                                                                                                                                                                                                                                                                                    Query Match 15.5%; Score 86; DB 14; Best Local Similarity 94.4%; Pred. No. 0.038; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                       ; LOCATION: (1)..(18)
; OTHER INFORMATION: HUMAN GENETIC ORIGIN US-10-142-238A-9
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OTHER INFORMATION: HUMAN GENETIC ORIGIN
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
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ORGANISM: ARTIFICIAL SEQUENCE
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                                                                        SEQ ID NO 9
LENGTH: 18
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LENGTH: 18
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RESULT 15

US-10-142-238A-15

US-10-142-238A-15

Sequence 15, Application US/10142238A

Publication No. US20030087819A1

GENERAL INFORMATION:

APPLICATION TOWNERTION:

TILLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES

FILE REFERENCE: 1B-1705

CURRENT APPLICATION NUMBER: US/10/142,238A

CURRENT APPLICATION NUMBER: US/60/289,944

PRIOR PILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PATENTIAL SEQUENCE

LENGTH: 18

TYPE: PRT

NAME/KEY: PEPTIDE

LOCATION: (1) . (18)

OTHER INFORMATION: HUMAN GENETIC ORIGIN

US-10-142-238A-15
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14.9%; Score 83; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 0.078;
Matches 17; Conservative 0; Mismatches 1; Indels
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 18; Conservative 0; Mismatches 0; Indels
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Search completed: December 21, 2004, 11:46:57 Job time : 60 Becs

1 GEEMRDRARACVDALRTH 18

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Patent No. 5189451
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Sequence 5, sequence 75, Sequence 75, Sequence 75, Sequence 4, p
Sequence 2, p
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Sequence 845, Sequence 845, Sequence 845, Sequence 845, Sequence 845, Sequence 25, Sequence
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1 OKLHBLQEKLSPLGBEMRDR......SFKVSFLSALBEYTKKLNTQ 112
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Sequence 3,
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-710-749-1

US-09-147-875A-3

US-08-710-749-2

US-08-710-749-3

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US-08-147-875A-4

US-08-147-875A-5

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Gapop 10.0 , Gapext 0.5
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Match Length
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29 58.5 10.5 10.7 1 (18.0-4.74-513A-105 Sequence 105, App 1 1 58.5 10.5 10.5 10.7 1 (18.0-4.74-513A-105 Sequence 21, App 1 1 58.5 10.5 10.5 10.7 4 (18.0-4.74-513A-105 Sequence 21, App 1 1 58.5 10.5 10.5 10.7 4 (18.0-4.74-513A-105 Sequence 115, App 1 1 58.5 10.5 10.7 5 (10.7 5 10.7 5 10.7 5 10.7 5 10.7 5 10.7 5 10.7 5 10.3 10.5 4 (18.0-5.110-741 Sequence 115, App 1 1 58.5 10.5 10.7 5 (19.0-4.74-513A-105 Sequence 115, App 1 1 58.5 10.5 10.3 10.5 4 (18.0-5.110-741 Sequence 115, App 1 1 58.5 10.5 10.3 10.5 4 (18.0-5.110-741 Sequence 115, App 1 1 59.5 10.3 10.5 4 (18.0-5.74-757-51 Sequence 115, App 1 1 59.5 10.3 10.5 4 (18.0-5.74-757-51 Sequence 115, App 1 1 59.5 10.3 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51 Sequence 122, App 1 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-51) Sequence 123, App 1 59.5 10.2 10.5 4 (18.0-5.74-757-
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SEQ ID NO:4:
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Best Local Similarity 30.4%; Pred. No. 0.21;
Matches 28; Conservative 13; Mismatches 22; Indels 2
                                                                                   Score 86; DB 2; Length 64;
Pred. No. 0.025;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUDUIAL: UCS.
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,389
FILING DATE: 19920519
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PILING DATE: 19920512
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16787/168/DFBC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                  Sequence 7, Application US/07849389
Patent No. 5525493
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UHLEN, Mathias
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LASHLRKLRKRLLRDADDLQKKLAVYQAGARE 100
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                                                                                   Query Match
15.5%; Score 86; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 17; Conservative 0; Mismatches
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1800 Diagonal Road, Suite 500
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amin
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AMINO ACID
               MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-07-849-389-7
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
STATE: Virginia
COUNTRY: USA
TOPOLOGY: linear
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                                                   US-08-292-870-1
                                                                                                                                                                                                                                                         US-07-849-389-7
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24 ELDAKQAKLSKI-EELSDK----IDELDAEIA-----KIEKNVEDFKNSNGEQAEQY 70
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
APPLICANT: BECKER et al.

TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REPERENCE: 454112-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ## Sequence 1, Application US/08710749
## Patent No. 595508
## GENERAL INFORMATION
## GENERAL INFORMATION
## APPLICANT: Hollingshead, Susan
## APPLICANT: Hollingshead, Susan
## APPLICANT: Becker, Robert
## TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
## TITLE OF INVENTION: PROTEINS
## NUMBER OF SEQUENCES: 28
## CORRESPONDENCE ADDRESS:
## ADDRESSEE: Curtis, Morris & Safford
## STREET: 530 Fifth Avenue
## CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5182364

Patent No. 5182364

TITLE OF INVENTION: POLYPEPTIDE ANALOGS OF APOLIPOPROTEIN E

NUMBER OF SEQUENCES: 14

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/485,158
FILING DATE: 26-FEB-1990
                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
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Best Local Similarity
Matches 20; Conserv
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Becker, Robert

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Patent No. 6638516
GENERAL INFORMATION:
APPLICANT: BECKER et al.
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REFERENCE: 454312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT PILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%; Score 67.5; DB 2; Length 1 Best Local Similarity 27.2%; Pred. No. 4.9; Matches 22; Conservative 15; Mismatches 31; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/710,749 FILING DATE: 20-SEP-1996 CLASSIFICATION: PATORNEY AGBNT INFORMATION: NAME: Frommer willing
                                                                                                                                                          NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE FOCKET NUMBER: 454312-2074
TELEPHONE: (212) 840-333
TELEPHONE: (212) 840-313
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
STRANNBENESS: n/a
TOPOLOGY: linear
MONECULE TYPE: amino acid
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Sequence 10. 5955089
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Hollingshead, Susan
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Best Local Similarity 26.7%,
Best Local 23, Conservative
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US-08-710-749-2
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Sequence 5, Application US/08777708C
Patent No. 6159934
GENERAL INPORTION:
TITLE OF INVENTION:
TITLE OF IN
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                 STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Jam PC compatible
COMPUTER: Jam PC compatible
COMPUTER: Jam PC compatible
COMPUTER: Jam PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-58P-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 12.0%; Score 66.5; DB 2; Local Similarity 27.2%; Pred. No. 6.3; ne 22; Conservative 15; Mismatches 31;
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12.0%; Score 66.5; DE
Best Local Similarity 32.9%; Pred. No. 6.5;
Matches 23; Conservative 10; Mismatches
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 EDLAAKQAELEKTEADLKKAV 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 101 amino acids
TYPE: amino acid
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MOLECULE TYPE: amino acid
US-08-710-749-2
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CRGANISM: Rattus norvegicus
US-08-777-708C-5
APPLICANT: Becker, Rober
TITLE OF INVENTION: STRA
TITLE OF INVENTION: PROT
NUMBER OF SEQUENCES: 28
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                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: USA
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Matches
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                  10; Gaps
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APPLICANT: DYER, CHERYL A.; CURTISS, LINDA K.; SMITH, RICHARD TILLS OF INVENTION: POLYPEPTIDE ANALOGS OF APOLIPOPROTEIN E NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/395,732

FILING DATE: 18-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.6%; Score 64.5; DB 6; Length 70; Best Local Similarity 27.4%; Pred. No. 6.4; Matches 20; Conservative 12; Mismatches 32; Indels
                                                                                                                                                                                                                                            TITLE OF INVENTION: DIAGNOSTIC SYSTEMS AND METHODS USING POLYPEPTIDE ANALGGS OF APOLILPOPROTEIN E NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,363
FILING DATE: 18-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 485,158
FILING DATE: 26-FEB-1990
PRIOR DATE: 18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Indels
                                                                                                                                                                       5168045-4
;Patent No. 5168045
: APPLICANT: DYER, CHERYL A.;CURTISS, LINDA K.;SMITH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 65; DB 6
28.8%; Pred. No. 5.5;
cive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.8*
Matches 21; Conservative
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54 LLRDA-DDLQKRL 65
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                                                                   77 KPALEDLRQG 86
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OMALESILOG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 69
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5177189-3
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US-09-147-875A-4 'Sequence 4' Application US/09147875A 'Patent No. 6638516 'GENERAL INFORMATION:

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24 ELDAKÇAKLİSKL BELSDK ----IDELDABIA-----KLEKDVEDFKNSDGEÇAGÇY 70
                                                                                                                                                                                                                                                                                                                                                                                                                              2 KIHELOEKISPLGEEMRDRARAHVDALRTHLAPYSDELRORLAARLEALKENGGARLAEY
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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APPLICANT: BECKER et al.
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REFERENCE: 91312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                          34; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Briles, David E.
APPLICANT: Hollingshead, Susan
APPLICANT: Becker, Robert
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 28
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                               DB 4; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.2%; Score 62.5; DB 2;
Best Local Similarity 28.4%; Pred. No. 17;
Matches 23; Conservative 14; Mismatches 31;
                                                                                                                                                                                                                                                                                                                            Query Match
11.4%; Score 63.5; Di
Best Local Similarity 27.9%; Pred. No. 13;
Matches 24; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 HAKATEHLSTLSEKAKPALEDLRQGL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LAAAGEDLIAKKAELEKAEADLKKAV 96
                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08710749
Patent No. 5955089
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 454
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
: New York
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                              US-09-147-875A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-710-749-3
                                                                                                                                                                                                                              TYPE: PRT
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<u>ښ</u>

13; Gaps

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US-08-182-175A-57

Sequence 57, Application US/08182175A

Patent No. 555923

GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      2 KLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEY 61
                                                                                                                                                                                                                                                                                                                                                                   24 ELDAKQAKLSKL-EELSDK----IDELDAEIA-----KLEKDVEDFKNSDGEQAGQY 70
  TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
                                                                                                                                                                                                                                                     DB 4; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 77;
                                                                                                                                                                                                                                                                                             35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: E.I. du Pont de Nemours and Company 1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CIASSIFTCATION BOO
PILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
RELEPHONE: (302) 992-4929
TELEFRANE, (302) 992-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%; Score 59.5; D:
25.3%; Pred. No. 26;
:ive 15; Mismatches
                                                                                                                                                                                                                                                     Query Match
10.9%; Score 60.5; D
Best Local Similarity 26.7%; Pred. No. 28;
Matches 23; Conservative 15; Mismatches
                     FILE REFERENCE: 454312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                          62 HAKATEHLSTLSEKAKPALEDLRQGL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LAAAEEDLIAKKAELEQTEADLKKAV 96
                                                                                                                                                                  TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57:
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Best Local Similarity 25.33
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Wilmington
STATE: Delaware
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 10
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7 QEKLSPLGBEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHAKAT 66
                            | | | : | : | | | : | | 26 GSESGDNVRSSAGAVRDAGGAFGKREQAEERYFRARAKEQLAALKKHHENEIS-HHAKE 84
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                                                                                                                                                                                                                Sequence 4. Application US/08893042
Fatent No. 5906923
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL ATPASE INHIBITOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 62.5; DE 27.5%; Pred. No. 19; tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEASESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,042
FILING DATE: Herewith
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0134 US
                          30 QAKLSKL-EELSDK----IDELDAEIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-147-875A-5
; Sequence 5, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
                                                                                                             77 EDLIAKKAELEKAEADLKKAV 97
                                                                                 67 EHLSTLSEKAKPALEDLROGL 87
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85 IERLQKBIERHKQSIKKLKQ 104
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 TEHLSTLSEKAKPALEDLRQ 85
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Best Local Similarity 27.5%;
Matches 22; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GEEMRDRARAHVDALR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRANGE
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 109 amino acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                            US-08-893-042-4
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